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(54) Title: **GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES**

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
15 survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

20 Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
25 new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
30 into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and
5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
10 libraries and

c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences
15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by
20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particularly useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ; SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
10 SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14 ;
SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

25 The invention relates also to a method of detecting differentially expressed genes correlated with a cancer comprising detecting at least one library of polynucleotide sequences as above defined or of products encoded by said library in a sample obtained from a patient.

30 A particular embodiment of the invention relates to a polynucleotide library of corresponding substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets 1 to set 212 as defined in table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from antracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJII BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>): Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software.

5 Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were
10 measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median
15 values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with
20 means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors
25 was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

30 Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF β 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

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the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFBR3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

25 Gene expression profiles were able to make this discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes
15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region Y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, subfamily b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (Li-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRV (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pi (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDNP2	19	actonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:328	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Ttk2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFB3	42	transforming growth factor, beta receptor III (TGFB3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	EphA2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	CAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 89		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	Jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1) (ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158992		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTRF	120	ciliary neurotrophic factor receptor (CNTRF)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	Jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (matrilysin 1) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST	rien		Image ?					
AW184517								

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

5 SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ
ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74;
SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID
No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET
10 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID
No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID
No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID
No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID
No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET
15 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:102) ; SET 42: (SEQ ID
No:103; SEQ ID No:104) ; SET 43: (SEQ ID No:105; SEQ ID No:106) ;
SET 44: (SEQ ID No:107; SEQ ID No:108; SEQ ID No:109) ; SET 45:
(SEQ ID No:110; SEQ ID No:111) ; SET 46: (SEQ ID No:112; SEQ ID
No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID
20 No:115; SEQ ID No:116; SEQ ID No:117) ; SET 49: (SEQ ID No:118;
SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51:
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No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127;
SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55:
25 (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID
No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ;
SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59:
(SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID
No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147;
SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID
30 No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154;
SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID
No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ;
SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164;
SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID
35 No:168) ; SET 69: (SEQ ID No:169; SEQ ID No:170) ;
SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173;
SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID
No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID
No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183;
SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186)
; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:200) ; SET 111: (SEQ ID No:263; SEQ ID No:264) ; SET 112: (SEQ ID No:265; SEQ ID No:266) ; SET 113: (SEQ ID No:267; SEQ ID No:268) ; SET 114: (SEQ ID No:269; SEQ ID No:270) ; SET 115: (SEQ ID No:271; SEQ ID No:272) ; SET 116: (SEQ ID No:273; SEQ ID No:274) ; SET 117: (SEQ ID No:275; SEQ ID No:276) ; SET 118: (SEQ ID No:277; SEQ ID No:278) ; SET 119: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 120: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET 121: (SEQ ID No:284; SEQ ID No:285) ; SET 122: (SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 123: (SEQ ID No:289; SEQ ID No:290) ; SET 124: (SEQ ID No:291; SEQ ID No:292) ; SET 125: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 126: (SEQ ID No:296; SEQ ID No:297) ; SET 127: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 128: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 129: (SEQ ID No:303; SEQ ID No:304) ; SET 130: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:
5 (SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID
No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450); SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
10 (SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

20 7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim
5 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10 12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each
15 one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET
20 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

25 30 wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
10 SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ; SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96 (SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258) ; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276) ; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296; SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166 (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401) ; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424; SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184 (SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

wherein said sequences are useful in classifying good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim 20 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequence sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

Normal Breast

Figure 1A

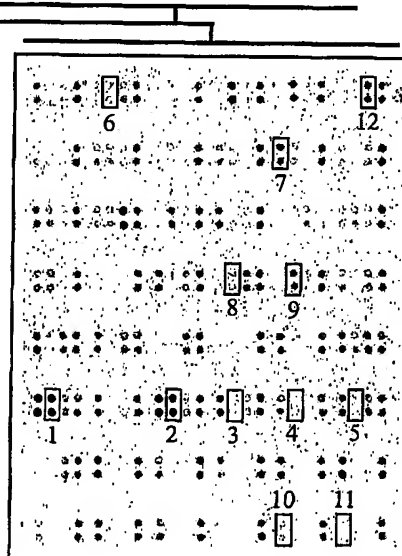
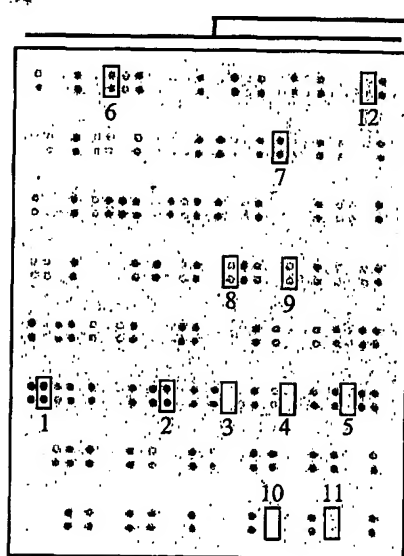
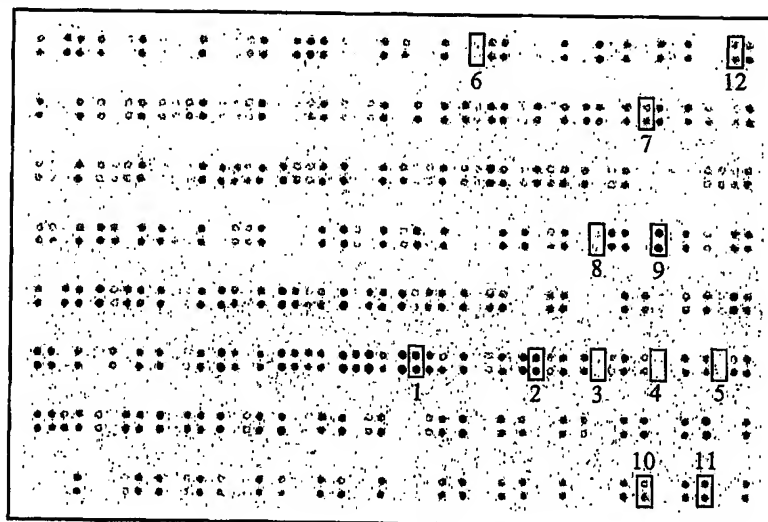


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

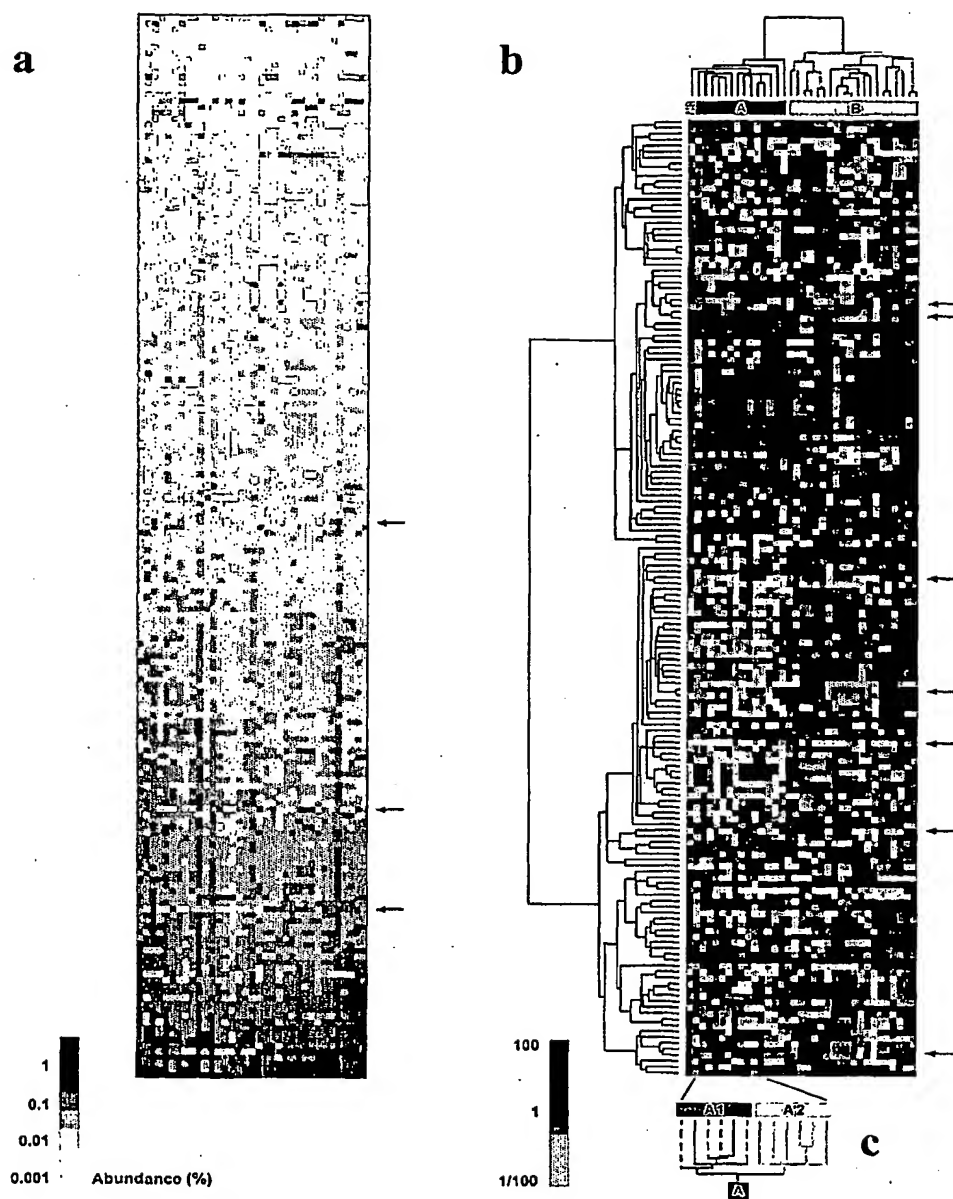


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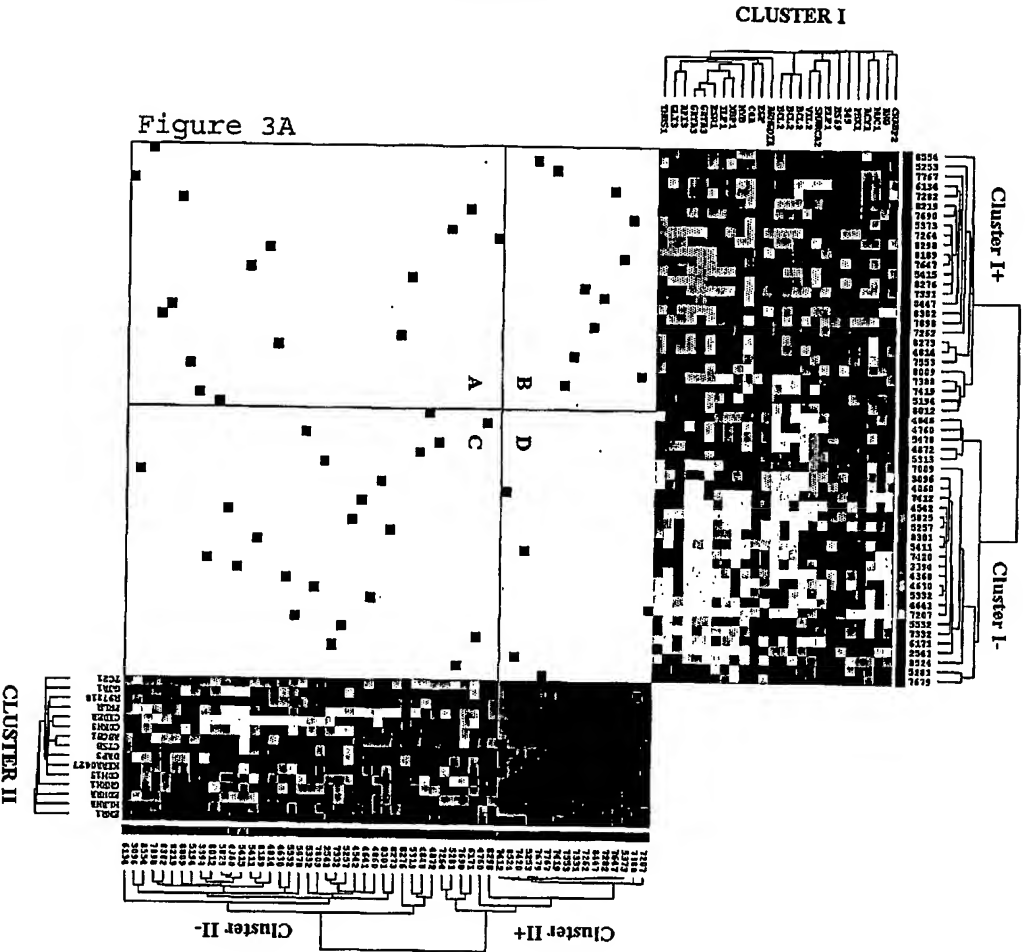


Figure 3C

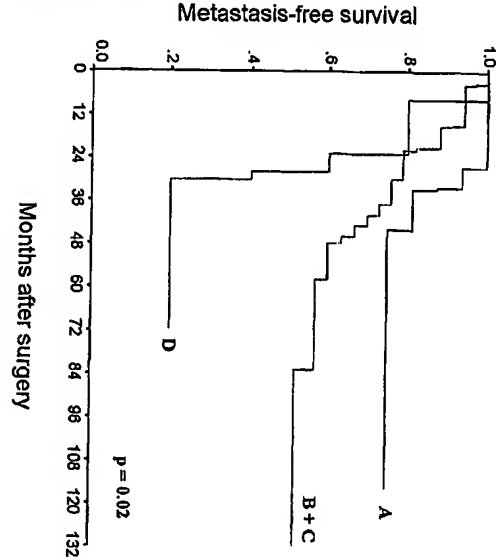


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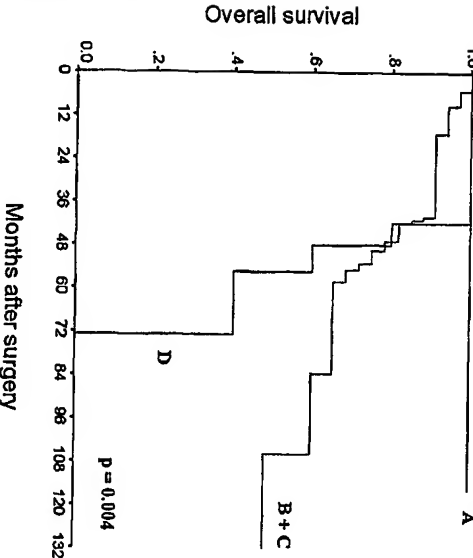


Figure 4

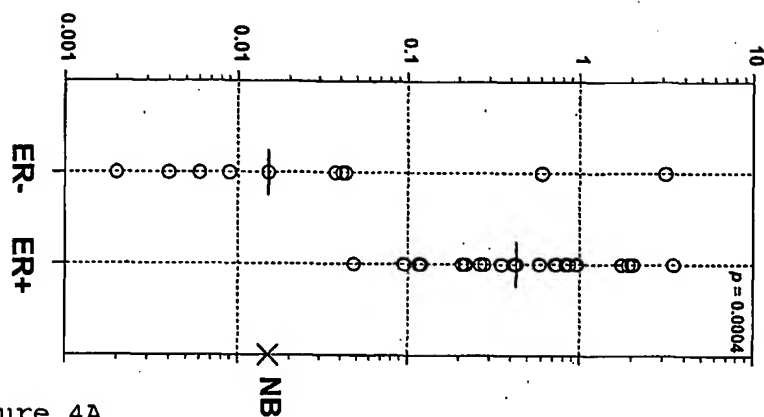


Figure 4A

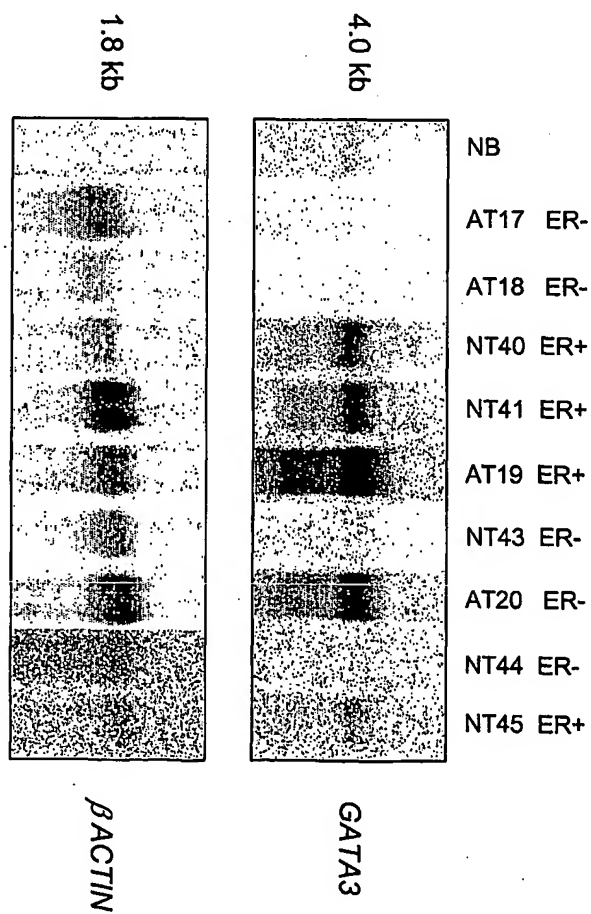


Figure 4B

SEQUENCE LISTING

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<110> François Bertucci
Rémi Houlgatte
Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

<120> cDNA arrays and their use for gene expression profiling.

<130> 10813PCT-December-2001-ipsogen

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ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
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acaatttgaa cacttgacgg ttgtcccttt taatttattt gaagtgtctat ttttttaaat 3300
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```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac aggggttnngc acattgccca ggatgggtctc aaactcctag agttgagcta 60
tccaccacc tttggcctnc caaagtgtct ggatcacagg cgtgagtcac tgnctccagc 120
acccatctgg aggtttctta aagcccaggc ccacgcgca gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctgttcc aggggccccca 240
ctttgaagaa cactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8

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aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tcctcttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt
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<210> 9

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(255)

<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9

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aaagacagtt tttgggtaat cttttncctt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc ccctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc
```

<210> 10

<211> 1325

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1325)

<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

gcagtagcag cgagcagcag agtccgcac g ctccggcgag gggcagaaga gcgcgaggga 60
gcgcggggca gcagaagcga gagccgagcg cggacccagc caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaacc 180
atccgccgcg cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcggagg agacctgcgc gccctcgggtg tcctacttca aatgtgtgca gaaggagggtc 300
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tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcc tgcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctctgtgtga acaagctcaa gtggaacctg 600
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aaagcttcat tctccttgtt gttggtgtt ttttcctttg ctctttcccc cttccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325

<210> 11

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11

atttgaagt caaagtotta ttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagtct ggcggctgaa ttccggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggtaatt gacctcgaga cgacctctct gccggttggt 300
ggtgatctcc aacgtcagcc agctcccag cgggtggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg antc tgttccttnt ttcctggact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt 449

<210> 12

<211> 4003

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

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gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg ccttggttgg 180
ggcacaaggt ggcaggatgt ctcaagtgtg cgaacttcag cagcttgact caaaattcct 240
ggagcagggt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
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ccgttttcat gacctcctgt cacagctgga tgaatcaaat agtcgctttt ctttggagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaaat 540
tctggaaaaa gccagagatg ttaat caggc tcagtcgggg aatattcaga gcacagtgat 600
gttagacaaa cagaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaagcaa 720
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gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attagggttg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
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```

ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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gcgaatgggt ccattctctc tcctgtactt tttccagaca cttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt ttacctttt tccttcctta tcaactgacac aaaaagtaga 3660
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```

<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 13

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ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
ataaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttattttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggac 60
tgttggcatg cagtgcctcc cagagaccaa cggtcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaat acttggaact cagccaacct ctggaacagt 180
attcacctag ttaccctgac ac aagaagtt ctgtgtcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaacatgcc ttcctcagta tccacacata aacgggcagt 300
gttttaaac atgaatgact gtgtctggcc tgncccaa acagggacag gcactggggg 360
aacctaggct acattnaggc aggggaggac ccttgccttc ccagngttt gttt 414

```

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<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson -weiss syndrome) (FGFR2) gene.

<400> 15
gagcgggcga gggagcgcgc gcggccgcca caaagctcgg gcgcgcggg gctgcatgcg 60
gcgtacctgg cccgcgcgcg cgactgctct c cgggctggc gggggcgcgc cgcgagcccc 120
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cccaccgcag gctgaaggca ttgcgcgtag tccatgcccc tagaggaagt g tgcagatgg 540
gattaacgct cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
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ggagaagatt tatgtcagca cactctaca gagcacaat gcagtatata ggtgctggat 3540
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atatacaaaa caattaatca tttatagttt tttttgtaat ttaagtggca tttctatgca 3840
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aaagagaata tttacaatat atgactaatt tggggaaaat gaagttttga tttatttgtg 3960
tttaaatgct gctgtcagac gattgttctt agacctcct a aatgccccat attaaaagaa 4020
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cccactcact ttgcaatagc cgtgcaagat gaatgcagat tacactgatc ttatgtgtta 4560
caaaattgga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
tctacagata ttaatgttaa caagaca aaa taaatgtcac gcaactt 4667

```

<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct ccaaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaatac tgatttggta aattaacccc acttctcata 180
gtttaattgg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg ggtcctgag gctgctgggg gtgatccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt ttttcccgag tctttgggag ttgttcccta ctgtggggct 360
acttataggg gtagggcccc ccaaatccct cacacttagg tcggccctgc tggttgcgtg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacc attttctggc 480

```

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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt ttacagaat 60
aaatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttgttc ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc cttgggtcgt cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggccccc cagcgtgtat gc tatecttt cgggggtggg 300
cattcgctca ttaattcggg ccagncctt cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttgagcac tataccaca aactgtccg aggggtgctt tatttctaca gttaccctgc 60
agtttgtaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagcca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gcccacaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcataaata tcaggcagtt taactgttct ccacaccctt actgggcttc 300
caaactttat gggatgtttt cacatgggtc ttgacctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tggntcaaca ttatggntct ggatggacgg aactgatttt 420
ctggatgat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnttagttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

13/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```

gggccaccct tagcagcggg cgcggtcggg gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cgggtgggccc tcgtcctgtc agtggcgctg gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggtgacggc ctccgggcag ctaaggctgc ccgaggagaa ggcggcggcc gcggcgtagg 240
cgcacgtccg gcgggctcct ggagcctgga ggaggccgag gggaccatgt ccgggaggcg 300
cttcacacct tccaccaccg accgcgtcat caa agctgtc ccctttcctc caacccaacg 360
gcttactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagt 660
tgtgtgtgat ttatggagtt taaagattaa tcatcccaaa acattgtttc tgcttcgggg 720
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gaaaatgaaa agcaactcaa aacaacttca acctggaggt gcatttataa ttcagtctgc 1920
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aaaaagtgca tctgttttgt ttttcccttt tttctccata attttaagaa atgaatctga 2040
ttgttgtaaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttggaac cctcaaacct gggtttctga cccc 2134

```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

<400> 20
atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttgtg caatggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttgngaataa atttntccaa 240
aaaaacca 248

<210> 21
<211> 427
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(427)
<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21
taagatacga acgagaaacc tgatttattg ctcatccttc ccttgccctcc ctaatggcaa 60
gcaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggta tattttaaag 180
tagaataaca catgctgagt gtaaactggg ctttggattg gtcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300
aaactggcta tgtggtagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420
cctttga 427

<210> 22
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(294)
<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22
tttcttgttt ttcttttttt tttccgaaa ccaactgccc tccactgact gccctgtac 60
cacatcaaac agtctcctct cctccacgcc tccgggtctt gggaagtctc acctcactga 120
tttcacgtag aaaagaaggc ggaggccagc agcgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gtttgaccgt gaacccctt cagttcgtg tctcctccg ccccccccc 240
tagctccgc tgctggnttc caacggggtt ntccgggtcat ttcctagcgc cggc 294

<210> 23
<211> 362
<212> DNA
<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttggg tttgttttat tttgcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgctgatg aagacagaag 180
gtctccgggt gacgaatttg gccgatggag nat gtttttg gggaacgccg ggactgagag 240
actccacggc agggcgaatt cccgtttggg gctttttttt tcctccctct ttttccctt 300
gccccttttg canccggngg agggagntgt tnaaggggag ggagggccag ccagtgttga 360
cc
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362

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```
ttccccagca ttcgagaaac tcctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaact gcagcgcggt gagagagcga gagagagagg gagagagact ctccagcctg 120
ggaactataa ctctcttcgc agaggcggag aactccttcc ccaaattctt tggggacttt 180
tctctcttta cccacctccg cccctgcgag gaggttgagg gccagttcgg ccgccgcgcg 240
cgtcttcccg ttccggcgtg gcttgcccg gggaaccggg agggcccgcc gatcgcgcg 300
cggccgcgcg gagggtgtga gcgcgcgtgg gcgccgcgcg agccgaggcc atggtgcagc 360
aaaccaacaa tgccgagaac acggaagcgc tgctggccgg cgagagctcg gactcggggc 420
ccggcctcga gctgggaate gcctcctccc ccacgcccg ctccaccgcc t ccacgggcg 480
gcaaggccga cgaccgcagc tgggtcaaga ccccgagtgg gcacatcaag cgacccatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccagca 600
tgacacaacg cgagatctcc aagcggctgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc ttctattoga gaggcggagc ggctgcgcct caagcacatg gctgactacc 720
ccgactacaa gtaccggccc aggaagaagg tgaagtccgg caacgccaac tccagtcct 780
cggccgcgcg ctctccaag ccgggggaga agggagacaa ggtcgggtggc agtggcgggg 840
gcggccatgg ggccggcggc ggcggcgga gcagcaacgc ggggggagga ggcggcggtg 900
cgagtggcgg cgccgccaac tccaaaccgg cgcagaaaaa gagctgcggc tccaaagtgg 960
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ccgcgcctct gctgcccttg ggcgcgcgcg ccgaccacca ctgcgtgt ac aaggcgcgga 1140
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tgcgcgcgcg ctgcgccgc ccgtccagcg cgcctcgca cgcgtcctc tcggcctcgt 1500
ccaactctc ctcttctctc tcctcgggct cctcgtcctc cgacgacgag ttcgaagacg 1 560
acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
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cgctcgtcggc gctcgaccgg gacctggatt ttaacttcga gcccggtcc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa gggc gcgcaggcag ggagaagggc 1800
cggggggggg aggagaggag aaaaaaaaaa tgaaaaaaaa aaacgaaaag gacagacgaa 1860
gagtttaaag agaaaaggga aaaaagaaag aaaaagtaag cagggctcgt tcgcccgcgt 1920
tctcgtcgtc ggatcaagga gcgcggcggc gttttggacc cgcgtccca tccccacct 1980
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aggggagacc tgtgattgtt gttattgatg ttgttgttga tggcaaaaaa aaaaagcgac 2100
ttcagatttg cttccctttg cttgaagaga cccctcccc cttccaacga gcttccggac 2160
ttgtctgcac cccagcaag aaggcgagtt agttttctag agacttgaag gacttcccc 2220
cttctgcat caccaccttg gttttgtttt attttgcttc ttggtcaaga aaggagggga 2280
gaaccagcg caccctccc cccctttttt taaacgcgtg atgaagacag aaggctccgg 2340
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cggcgctgc tgggcctccg cttcttttc tacgtgaaat cagtggagt agacttcca 2700
gaccccgag gcgtggagga gaggagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtt ttcggaaaaa aaaaagaaa aaaaggg 2797

```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5
(RNF5) gene.

<400> 25

```

acgggggccc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacaaggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtccgcg tttatgggag agggagccag aagccccagg 240
atcccagatt aaaaactcca ccccgcccc aggcc agaga ccagctccgg agagcagagg 300
gggattccag ccatttggtg ataccggggg cttccacttn ttcatttggg gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

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atggcagcag cggaggagga ggacgggggc cccgaagggc caaatcgca gcggggcggg 60
gcgggcgcga ccttcgaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

```

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gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgagggg gccagaagcc ccaggatccc agattaaaaa ctccaccccg ccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
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catgagcctt tccgccgggg tacagggtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt cctcttctct gtttctcgcc atcttcttct ttttttggct gctcagtatt 540
tga 543

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

gccgtggggg gggaaagtgg gaag gtggag ttttccccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggaggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggctctgg 240
ctgggttggg gggtcagctc ctccctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatntn acatagagga tttcgtcagg ctccctggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttcccn caactctnta aaacttt 397

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggcg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agatttttgg gagnacacac ttttaagggc tttncctt 418

<210> 29

<211> 5015

<212> DNA/RNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

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gagtgaggatt ctggaggaat gtttaccaga cacagagccc agagggacag cgcccagagc 60
ccagatagag agacacggcc tcaactggctc agcaccaggg tccccttccc cctcctcagc 120
tccctccctg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggt gccctggct ctggcctggt gggcggaggc aaagggggag ccaggggagg 240
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gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcacaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cgcccgcgtg ccccctcccc 420
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gatgggcagg gtcccgtagg cctggtgctt ggcgctgtgc ggctgggctg gcatggcccc 540
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```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)
gene.

<400> 30

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gaatggcaca ccctactggc tgg ttgcaa ctcctgggaa actgactggg gtgacaatgg 120
cttctttaaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggct tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttattc tttaagttca cgtaagggat 300
acaagttttc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttccaagg gaggaccaag ttctggggt aacattcccc agcctnttgg ttttaacagtt 420
gncaggacag ggcctgtt

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439

20/292

<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
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ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

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gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagecagg ga cagccccccc ccacgccag 240
cctccgtctg agggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggagg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggcttncca cattttcca cagcgggtaca 480
agttagtttt tg 492
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<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

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ctggcactta aggttcgcta tcttgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggctca tggcttctac gatgagtgcc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg caggggggcc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330
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<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cgccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
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tcagagtagg tggcgacgtc cctgagacca actacctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaagggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```


22/292

```

tctacgatga gtgcctgcgc aagtaagggt cggtagactgt gtggcgctac tgcactgaga 540
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aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1429

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<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)
gene.

<400> 35

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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatatc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcctac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggncac tcccngttg gatgggnttt gggggaggag ncctgntggg 480
gntttttccc at 493

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<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

<400> 36

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ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgctgg ggcagcagca 120

```

23/292

gcagggggag gtnntgggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaaggga aggggcacgg ccttngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

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ggcagcagcg ccctcccaga ggcctacctt caagcagctg gtggaggcgc tggacaaggt 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctggtgggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctcttccct ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

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cccattcctg aggcggggct cccggccaac accacagccg tgggtggcag cgacgtggag 960
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24/292

```

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ctggtctcct gcgcctacca ggtggccgga ggcattgcagt atctggagtc ccggaagtgt 1980
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gcccttgccc ttggagctgc cgtgcctgtg tctgatggc ccaaatgtca gggttctgct 2760
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tttttttgaa ataaa

```

3015

<210> 39
 <211> 252
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(252)
 <223> 3' terminal sequence. ectonucleotide
 pyrophosphatase/phosphodiesterase 2 (autotaxin)
 (ENPP2) gene.

```

<400> 39
gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtggt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta

```

252

<210> 40
 <211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

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gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gatctttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc                                     382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
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ggagtcaata tctgcttagg attcaactgca catcgaatta agagagcaga aggatgggag 120
gaaggtccctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgctg ccatgacttt gatgagctgt gtttgaagac agcccgtgcg 300
tgggagtgtg ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtggg ttgcaaagga 420
gagtcgcatt ggggtgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc cttgtggcac aactctccc 600
taccatgaggc cgggtgtacc aactaaaacc tttcctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgatcctgt atttgatgcc 720
acttttcac tgcgagggcg agagaaattt aatcatagat ggtggggagg tcaaccgcta 780
tggattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgtcatc 840
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ggaatggaag atgtcacatg tgatagaact gagttcttga gtaattacct aactaatgtg 1140
gatgatatta ctttagtgcc tggaaactcta ggaagaatc gatccaaatt tagcaacaat 1200
gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
ttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgcaa caacagaaga 1320
```

26/292

```

attgaggata tccatthatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
gtttataaga aaccatcagg aaaatgcttt ttccagggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
ccagctccta ataattgggac ccatggaagt ttgaatcatc tcctgcgcac taataccttc 1620
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cgacctgcag tgctttatcg gactagatat gatattctat atcacactga ctttgaaagt 1860
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aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
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agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tccngactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcacttga gaagagggag agcaagggaag tccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcg tggntttcct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc tgtagggcag gaaggccagc ccctcaaacg ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctag gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3 (p65))
(RELA) gene.

<400> 43

```
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gctccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggc a ccaaggacc 240
ctcctcaccg gcctcaccgc cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccggac cgctgcatcc acagtittcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcat ccagaccaac aacaaccct 420
tccaagtacc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgccggac ccatcaggca ggccccctcg cctgccgcct gtcccttctc 540
atcccatctt tgacaatcgt gccccaaca ctgccgagct caagatctgc cgagtgaacc 600
gaaactcttg cagctgcctc ggtggggatg agatcttct actgtgtgac aaggtgcaga 660
aagaggacat tgagggtgat ttcacgggac caggctggga ggcccagggc tccttttcgc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac cctccctac gcagaccca 780
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caggaggcat agtttttagt gaacaatcaa agcacttga ctcttgcctt ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgtcatgg gaagaagcgc acgctgaagg ggtccattga gctctcccga 240
attcaaatgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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attcagatat gtttgaacaa ttcttaaggc tacaaaacag aacatagaaa aataaacagg 120
aataatattca aactttacaa aaagtgatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttacaa gtaacatcac aaatgctcac 240
atcttcacat gctcttaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaagtgg ccgcttccca gcattaagac atgcaccac cctctttcta agattttcta 420
aacttgtatt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat tttaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaaata gttagccaa atatcattct ctacagctac ctttaagtaa agacaaaaca 660
tttacctcat ctaaaaatga aggtaaaacg aaagaggcaa aaataaataat tgctagtttc 720
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gaggtgatgc ccaaggtgca ccacctttca agaactggat catgaacaac tttatcctcc 2040
```

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ctgtacagcc tgacactgta tgggctgcga ggacccaca aggccagac catccaggga 11580
accgccccga ccctcagccc agttctggag agccccgctg acctccaatt cagtgaatc 11640

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```

agggagacct cagccaaggt caactggatg cccccacat cccgggcgga cagcttcaaa 11700
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gtaccgcg 13268

```

<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 48

```

ttttgcagct tgtgcacttc ttttattatt aaatatataa gcagcttccat atctttttaa 60
tagatatatta aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttcccatttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttcact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

```
ggcaccgaggc gagctctgac tgaagatggg cctttgaaat ataggtatgc acctgaggtt 60
gggggagggt ctgcactccc aaaccccagc gcagtgtcct ttccctgc tg ccgacagaac 120
ctggggctga gcaggttata cctgtcagga gccctgggac tgggctgcat ctacgcccc 180
cctggcatgg tatccagctc ccatccactt cttcaccctt ctttcctcct gaccttgggt 240
caacagtgat ggaccttcca actcttcacc caccctctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagc 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) .
(CSF1) gene.

<400> 50

```
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caccacgcga gcgagcgagc gacgcagggc ggccgacgcg ccgggcccgg acccagctgc 120
ccgtatgacc gcgcccggcg ccgcccggcg ctgccctccc acgacatggc tgggtccct 180
gctgttgttg gtctgtctcc tggcgagcag gactatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggctgattg acagtcagat 300
ggagacctcg tgccaaatta catttgagtt ttagaccag gaacagttga aagatccagt 36 0
gtgctacctt aagaaggcat ttctcctggt acaagacata atggaggaca ccatgcgctt 420
cagagataac accccaatg ccatcgccat tgtgcagctg caggaactct ctttgaggct 480
gaagagctgc ttcaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
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ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagcttg ctgaatgctc 660
cagccaagat gtggtgacca agcctgattg caactgcctg taacccaaag ccatccctag 720
cagtgaaccc gctctgtctt cccctcatca gccctcgcgc ccttccatgg cccctgtggc 780
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acatgagagg cagtccgagg gatcctccag ccgcagctc caggagtctg tcttccacct 1620
gctggtgccc agtgtcatcc tggcttctgt ggcgtcggg ggcctcttg t tctacaggtg 1680
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```

gaggcggcgg agccatcaag agcctcagag agcggattct cccttgagc aaccagagg 1740
cagccccctc actcaggatg acagacaggt ggaactgccg gtgtagaggg aattctaaga 1800
cccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
cccggacaca gtactccaga tgttgtctga ccagctcaga gagagtacag tgggactgtt 1920
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taactttttt aaccaaagtg cagtttatgt tcacctttgt taaagccacc ttgtggtttc 2160
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ctccagttg tgctcctgc acattgatga gtgcctgctg ttgtctttgc ccatgttgtt 2280
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ctctccccc tcccacccaa gccacagcc agcccatcag gaagccttc tggtctctcc 2400
acaaccttct gactgtctt tcagtcatgc cccctgctt tttgtattg gctaatagta 2460
tatcaatttg cactt                                     2475

```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```

atcngttgaa tagttgattc catacatttc cagg tcttga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacgggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactgggtc ctggtaagtt tgtgctggtc catcactctt tgagggatca nccgctcaga 180
gctgagggtac ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctggggt gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc                                     397

```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

```

ggacgaggca gggcggggcg gcgtctaaag ggttctgctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagtta ccacctgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcagggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgccaggga ggtcagggaag gagaatcccc tccagttcaa 360

```

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gttcgggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

aggcagggcg ggcgggcgct ctaagggttc tgctctgact ccagggtggg acagcgtctt 60
cgctgctgct ggatag tcgt gttttcgggg atcgaggata ctcaccagaa accgaaaatg 120
ccgaaaccaa tcaatgtccg agttaccacc atggatgcag agctggagtt tgcaatccag 180
ccaaatacaa ctggaaaaca gctttttgat cagggtggtaa agactatcgg cctccgggaa 240
gtgtggtact ttggcctcca ctatgtggat aataaaggat ttctacctg gctgaagc tg 300
gataagaagg tgtctgcccc ggaggtcagg aaggagaatc ccctccagtt caagttccgg 360
gccaaagtct accctgaaga tgtggtgag gagctcatcc aggacatcac ccagaaactt 420
ttcttctccc aagtgaagga aggaatcctt agcgtatgaga tctactgcc ccctgagact 480
gccgtgctct tggggtccta cgctgtgcag gccaaag ttg gggactacaa caaagaagtg 540
cacaagtctg ggtacctcag ctctgagcgg ctgatccctc aaagagtgat ggaccagcac 600
aaacttacca gggaccagtg ggaggaccgg atccagggtg ggcattgcga acaccgtggg 660
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atacacctta ttaatgatca gctatatact atttatatac aagtataat acagattttg 2580

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aacattagtt ttaaaaaggg aaagttttgt tctgtatatt ttgttacctt ttacagaata 2640
aaagaattac atatgaaaaa ccctctaaac catggcactt gatgtga tgt ggcaggaggg 2700
nagtgggtga gctggacctg cctgctgcag ctgcagtcac gtgtaaacag gattattatt 2760
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gccactcat tccttctcgt gactgcttt ctccttcaca gctaagatgc catgtgcagg 3000
tggattccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa

```

3064

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis coli (APC) gene.

<400> 54

```

tgcataaata ccaatttttc cctgatgtaa gtttagtcag tttataatct agaaatgatt 60
gataacagca atatatcata ttttctatct gtagtggtca ttattttaag acaagcaata 120
attaaaggaa gttgggatgg gatgctactt taaatacatg taaaacatac tgtacaaaca 180
tacttggctt tactattttt ttctaacca tcaagagtgc ctcccaaat aa gnccagtg 240
aagacaaagt atactatcaa atatgggctt ccnggaacaa aaacctctt aacaagggnt 300
ccaaacccta tttacaaaaa tttcccggt cttttaaggt ttccatttgg aaaccaaaat 360
gtctatatgg ccggttggtg attancatgg ggnttttctt gggnttcctt ctcccnct 420
cttttaacc ggtgg

```

435

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis coli (APC) gene.

<400> 55

```

agaaaaatgaa ttttctccca caaatagtac ttctcagacc gtttcctcag gtgctacaaa 60
tggtgctgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
tgtttgggtg agaattgagg actgtcccat taacaatcct agatctggaa gatctccac 180
aggtaatact ccccgggtga ttg acagtgt ttcagaaaag gcaaatccaa acattaaaga 240
ttcaaaagat aatcagggca aaacaaaatg tggggtaatn ggcagtgttc ccatgncgta 300
ccgtgggggt tnggaaaatc gcctggaact cctttatttc aggtgggatg cccctgacca 360
aaaaggganc ttnnggttna aaccggggnc aaattattcc tgttccctgt tttc

```

414

<210> 56

<211> 10383

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(10383)

<223> adenomatosis polyposis coli (APC) gene.

<400> 56

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agttgttaaa gcaagttgag gcaactgaaga tggagaactc aaatcttcga caagagctag 120
aagataattc caatcatctt acaaaactgg aaactgagga atctaataatg aaggaagtac 180
ttaacaact acaaggaagt attgaagatg aagctatggc ttcttctgga cagattgatt 240
tattagagcg tcttaaagag cttaacttag atagcagtaa tttccctgga gtaaaactgc 300
ggtaaaaaat gtccctccgt tcttatggaa gccgggaagg atctgtatca agccgttctg 360
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ttgacaaaga agaaaaggaa aaagactggt attacgctca acttcagaat ctactaaaa 540
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<210> 57

<211> 404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(404)

<223> 5' terminal sequence. mucin 1, transmembrane
(MUC1) gene.

<400> 57

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cgatcgtagc ccctatgaga aggtttttng caggtaatng gttggcagca gcttttttta 360
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<210> 58

<211> 1721

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1721)

<223> mucin 1, transmembrane (MUC1) gene.

<400> 58

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<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth
factor 2 (somatomedin a) (IGF2) gene.

<400> 59

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<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth
factor 2 (somatomedin a) (IGF2) gene.

<400> 60

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<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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gtttctggggc tgggtgggga tccctcattt cccatgttaa gcttgaggaa gagatttcag 360
 ggtaggctcc ctgcaggga actacttgtc cctcaacttt nggcctccca tagcatattt 420
 tnaaagccag naagggtttt ttaacccctt ntttgggaag cccgattggc att 474

<210> 63
 <211> 457
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(457)
 <223> 5' terminal sequence. egf-like module
 containing, mucin-like, hormone receptor-like
 sequence 1 (EMR1) gene.

<400> 63
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 gggttaaagt cttttcttgc tttcaaata gctatggagc cacagttgag gacagtagtt 180
 tcctgcagga gcctaccctg aaatctcttc tcag cttaac atgggaaatg aggatccac 240
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<210> 64
 <211> 3149
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3149)
 <223> egf-like module containing, mucin-like,
 hormone receptor-like sequence 1 (EMR1) gene.

<400> 64
 ctaaagtttt tttctttgaa tgacagaact acagcataat gcgtggcttc aacctgctcc 60
 tcttctgggg atgttgtgtt atgcacagct gggaaggga cataagacc acacggaaac 120
 caaacacaaa ggtaataaac ttagagaca gtaccttggt c ccagcttat gccacctgca 180
 ccaatacggg ggacagttac tattgcactt gcaaacaagg cttcctgtcc agcaatgggc 240
 aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300
 cccagccctg tggctctaac tcactctgca aaaacctgtc agggaggtag aagtgcagct 360
 gtttagatgg tttctcttct cccactggaa atgactgggt cccaggaaaag ccgggcaatt 420
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 tgtgccccat caattcaaca tgcaccaaca ctctgggag ctacttttgc acctgccacc 780
 ctggctttgc accaagcagt ggacagttga atttcacaga ccaaggagtg gaatgtagag 840
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gcctgacaca gagaacctct caataaatga tttgtgcct gtctgactga tttaccctaa 3120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

```

<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

```

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tgaaggttta cagactgggtc aaggaaggac gaacagagag aatgggtgtc gaggggtcac 120
atcccgtgga ggggtggcggg gctcctggcc tcgtctgggt gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaagcca ccaggccttg gggagcaggg ctttgccaag 240
caggccgcct cgga gaaaaa caatgactaa ctatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

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ccccggggcn agggngngaaa gcaattncaa agccttttagg aaatttcaat tt

412

<210> 66

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 5' terminal sequence. kiaa0427 gene product
(KIAA0427) gene.

<400> 66

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gggatngagt tagttcattt tt 442
```

<210> 67

<211> 5737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5737)

<223> kiaa0427 gene product (KIAA0427) gene.

<400> 67

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<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

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gccactctgc aatgtccctg gggnccgatg aggtaacaaa tgcaccccg ggaccagag 300
gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377

```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

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gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgcccaggg gaaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgcagga caaagggcc cca gaggagg aagccctacc cntgggacac 240

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agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

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ctttaaaaaa aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaatgtga gtttcaatcc tgaaagtttc 60
ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120
ctgcaagata cgtttcctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
ggagattcat ccttcacatg cctgggctng ggaatgttca gtgcatgtga cgccctatt 300
tttctccttt t 312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctagggtaca acttttggca tggt tttttc 60
tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
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atgtggggcc ctggtggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttgagga 360
aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggctccttt 420
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taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
tagtcaggg gagatggatc ctatcttact aaccatcagc attttgagtt ttttctctgt 780
cgctctgttg gtcattcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg 840
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tggcaagaat gggcctcatg tgtaccagga cctcctgctt agccttgga ctacaaacag 1260
cacgctgccc cctccatttt ctctocaatc tggaatcctg acattgaacc cagttgctca 1320

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gggtcagccc attcttactt ccctgggatc aaatcaagaa gaagca tatg tcaccatgtc 1380
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aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
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<210> 73

<211> 236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(236)

<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73

taaaaacaat agaaaaaat caactttaaa aagcaaatg tacttaaata aaaaaatta 60
gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt ttatttaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaactt taaaattttt taaaanccaa ttcttaaata ccaaactctgt taaggg 236

<210> 74

<211> 413

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(413)

<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74

acgtctccac acatcagcac aactacgcag cgctccctc cactcggaag gactatcctg 60
ctgccaagag ggtcaagttg gacagtgtca gagtctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccgaggt tgggaaaaca atgaaaaggc cccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggaggagacc aaaagttcat tttnttgaag 360
gagggnnttt ttttccgggn aacgacgagg aaccatttn aaacacaant ttt 413

<210> 75

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

53/292

<223> Description of Artificial Seq uence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

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acgcggggag gctattctgc ccatttggg acaattcccc gccgctgcca ggaccgctt 480
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cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
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gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttat gct taccatcttt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
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<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata -binding protein 3
(GATA3) gene.

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<400> 76

tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
ggggtccaga ttcagtgggt ggaacacaga caccacagtg agtcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggtcttt 260

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 77

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tctggtttct tcacttcctt ataagggcac caatcttatt cagagggtc tcacctcga 120
aataatcacg tcctcaaaaac cccaccttc taatattcta ataccatcac gtgagggtt 180
aggtttcaac ataagaattc ggtggtggtn ggggttnggg gagaggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaatc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctncgttt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc, ttnaggccan tccagggca 409

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

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ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tccccgcgag ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
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ttttaacatc gacgggtcaag gcaaccacgt cccgcctac ta cggaaact cggtcagggc 360
cacggtgcag aggtacocct cgaccacca cgggagccag gtgtgccgcc cgctctgct 420
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ccccgggaat ctacgcccct tctccaagac gtccatccac cacggctccc cggggccct 540
ctccgtctac ccccggcct cgtcctctc cttgtcgggg ggccacgcca gcccgacct 600
cttcaccttc ccgcccaccc cgccgaagga cgtctccccg gaccatcgc tgtccacccc 660
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gcccagacag atgaagctgg agtcgtccca ctcccgtggc agcatgaccg ccctgggtgg 78 0
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cattcagttg gcaaaaaaaaa aaaaa 2365
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<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

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ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgccct agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtgggg ctgttttcta tctgaggag 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgcccc 300
tgtggccgat cccanagtcc actnggat 328
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<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

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catgtctgggc gtgtcattga gaacccccgg gaggctctga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctccagcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
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agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatatt aagcattggt 42 0
tgattggc 428
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<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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gccagacttc ggaacgggtg tcctgctact cctgctgggg ctctccagg acaaggga c 180
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tgggggcagc ccaggcggtt tcacgcccc cacttt gtac agaccgagag gccagttgat 2160
ctgctctggt ttatactagt gacaataaag attatttttt gatac 2205

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
acagacagat aaagttccaa gtaaaacggt agctgctaaa aagggtatgt acttatattt 120
gattgagtta agcattggat agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
actatttgca tttttttatc ataaaacaat taaggagta taagtgtta taaggaggac 240
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta nttaaagct 300
gttgantttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
gene.

<400> 83

atggccaagt cgggtggtg cggcgcgga gccggcgtg gcggcgga cggggcactg 60
acctgggtga acaatgctgc aaaaaagaa gagtcagaaa ctgccaacaa aaatgattct 120
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
cttcgtctcg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
gatgaagatg taggaatgaa ttgcaggag gttacotttg tgccaggttt atacaagatc 300
tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
attaaagttt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
attccagtag tagaacacaa gtagagaaa gtttat gttc ctgctttaat tttggacag 480
cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacaggtg tcgtaatggt 540
tatggtgcaa aactttgtaa tattttcagt acaaagttta cagtagaac agcttgcaaa 600
gaatacaaac acagttttaa gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
aaaattaaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
aaatttaaga tggaaaaact tgacaaggat attgtggccc tcatgactag aagggcata 780
gatttggtg gttcgtgtag aggggtcaag gtcattgtta atggaaagaa attgcctgta 840
aatggatttc cgagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

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gaaaaaggat tccagcaaat cagcttttga aatagtattg caactacaaa aggtggacgg 1020
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 aacaaagctg gtgtatcagt gaaaccattt ca agtaaaaa accatatatg ggtttttatt 1140
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 cccaaaagtt ttgggtctaa atgccagctg tcagaaaaat tttttaaaagc agcctctaag 1260
 tgtggcattg tagaaagtat cctgaactgg gtgaaattta aggtcagac tcagctgaat 1320
 aagaagtgtt catcagtaaa atacagtaaa atcaaaggta ttcccaaact ggatgatgct 1380
 aatgatgctg gtggtaaaca ttccctggag tgtacactga tattaacaga gggagactct 1440
 gccaaatcac tggctgtgtc tggattaggt gtgattggac gagacagata cggagttttt 1500
 ccactcaggg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaaat 1560
 gctgaaataa ataataattat taaaatagtt ggtctacaat ataagaaaag ttacgatgat 1620
 gcagaatctc tgaaaacctt acgctatgga aagattatga ttatgaccga tcaggatcaa 1680
 gatggttctc acataaaaagg cctgcttatt aatttcatcc atcacaattg gccatcactt 1740
 ttgaagcatg gttttcttga agagttcatt actcctattg taaaggcaag caaaaaaag 1800
 caggaaactt ccttctacag tattcctgaa tttgacgaat ggaaaaaaca tatagaaaac 1860
 cagaaagcct ggaaaaataa gtactataaa ggattgggta ctagtacagc taaagaagca 1920
 aaggaatatt ttgtcgatat ggaaggcat cgcacttctg ttagatatgc tggctcctgaa 1980
 gatgatgctg ccattacott ggcathtagt aagaagaaga ttgatgacag aaaagaatgg 2040
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 ctcttctcaa actcagacaa tgaagatctc atac catctc ttgttgatgg ctttaaacct 2220
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 cagcctattg gtcagtttgg aactcggctt catgggtggc aagatgctgc aagccctcgt 2460
 tatattttca caatgttaag cacttttagc aggtactttt ttctgtctgt ggatgacaac 2520
 ctcttaagt tcctttatga tgataatcaa cgtgtagagc ctgagtggta tattcctata 2580
 attcccatgg ttttaataaa tgggtgctgag ggcattggta ctggatgg gc ttgtaaacta 2640
 cccaactatg atgctaggga aattgtgaac aatgtcagac gaatgctaga tggcctggat 2700
 cctcatcca tgcttccaaa ctacaaaaac tttaaaggca cgattcaaga acttggtcaa 2760
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 aatggaacag ataaaacacc agcatthaatt tctgattata aagaatatca tactgacaca 2940
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 ctgcataaag tttttaaaact tcaaactact cttacttgta attccatggg actttttgat 3 060
 catatgggat gtctgaagaa atatgaaact gtgcaagaca ttctgaaaga attctttgat 3120
 ttacgattaa gttattacgg tttacgtaag gagtggcttg tgggaatgtt gggagcagaa 3180
 totacaaagc ttaacaatca agcccgtttc atttttagaga agatacaagg gaaaattact 3240
 atagagaata ggtcaaagaa agatttgatt caaatg ttag tccagagagg ttatgaatct 3300
 gaccagctga aagcctggaa agaagcacaa gaaaaggcag cagaagagga tgaacacaa 3360
 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaga ttttaattat 3420
 attttaaata tgtctctgtg gtctcttact aaagaaaaag ttgaagaact gattaacag 3480
 agagatgcaa aagggcgaga ggtcaatgat cttaaaagaa aatctccttc agatctttg 3540
 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaaatctca agaacgagaa 3600
 gatgttctgg ctggaatgtc tggaaaagca attaaaggta aagttggcaa acctaagggtg 3660
 aagaactcc agttggaaga gacaatgcc tcaccttatg gcagaagaat aattcctgaa 3720
 attacagcta tgaaggcaga tgccagcaaa aagttgctga agaagaagaa ggggtgatctt 3780
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 gcaggagaag aggcattgac tccatcagtt cctataaata aaggtcccaa acctaagagg 3900
 gagaagaagg agcctggtac caga gtgaga aaaacaccta catcatctgg taaacctagt 3960
 gcaaaagaa tgaagaaacg gaatccttgg tcagatgatg aatccaagtc agaaagtgat 4020
 ttggaagaaa cagaacctgt ggttattcca agagattctt tgcttaggag agcagcagcc 4080
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 gatgatgaca ataattgatt agaggaattg catctcccat acaaatgat 4200
 ggggaagatg aatttgttcc ttcagatggg ttagataaag atgaatatac attttacca 4260
 ggcaaatcaa aagccactcc agaaaaatct ttgcatgaca aaaaaagtca ggattttgga 4320
 aatctctct catctccttc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgtttt taccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacgg agctgctaaa aagggaac cgtcttcaga tacagtcctt 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaaact tgactcggat 4560
 tcagaatttg gcattccaaa gaagactaca acacaaaaag gtaaaaggccg aggggcaaa 4620

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aaaaggaaag catctggctc tgaaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttccttac tgagccacct tctctgccac gaaccggtcg g gctaggaaa 4800
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa 4866

<210> 84

<211> 311

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(311)

<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

<400> 84

cacttttatt gaaatacaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggtcg ggctgcttgg ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatata ttgtcatgga cagtcgttct atgggtgggca tttgagcttt ggcccttgga 180
gtttcaaatg attgctgtac cttccgaaat acttctctta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t 311

<210> 85

<211> 1291

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1291)

<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

<400> 85

gctctttcca acgctgtaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggtg ttggaatccc tgggcaaaga tttcctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaacttaca gatgccctca 360
agctttgtcc tcatgaagaa ttcctgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaacaacac cgacacgcc ttgctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggtctgga ctatagtgtg gatgtagaag agaacttgac agccagggat atggagtcag 600
cgctgagggc atttgtacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gaggaatct gcggaactgt gcatgatgag aaaaaccag 720
atgtgtgtct ttatgacacc atcttccaga tattcaacaa ccgcaactgc ctcagtctga 780
aggacaaacc caaggtcatc attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctctc acagtcactc gagaacctgg 900
aggaagatgc tgtttacaag acccagctgg agaaggactt cattgctttc tgctcttcaa 960

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cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtag 1080
agcaatcatt tgaaactcca agggccaaag ctcaaagcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291

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<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 86

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tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggcgttg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttggnggaac ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctott gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga ccagtcctat ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319

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<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

<400> 87

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cgcagcaaac acatccgtag aaggcagcgc ggccgcga g agccgcagcg ccgctcgcgc 60
gccgcccccc acccgccgc cccgcccgc gaattgcgc ccgcgccct cccctcgcgc 120
ccccagagaca aagaggagag aaagtittgc cggccgagcg gggcaggtga ggagggtgag 180
ccgcgcggga ggggcccgc tcggcccgc ctcagcccc gccgcgcgc ccagcccgc 240
gccgcgagca gcgcccgc ac ccccagcgc cggccccgc ccgcccagcc ccccgccgc 300
ccatgggcgc cgcggccgc accctgcgc tggcgtcgc cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgc tcagctgct cccgggtgca ccgcgaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgc tcagtgaaga ggaagtggac tctggaaacg 480
acatttatgg caaccctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaaggatata gagtttatc acacggcccc ctctcggca gtgtgtgggg 600
tctcgttga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
gcaagatgca catcaccctc tgtgacttca tcgtgcc tg ggaacacctg agcaccaccc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgtacatc tcctccccgc acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900

```

cctgtgctg gtaccg cggc gggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctggtccagc tctgacatcc ctctctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta tttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcac ggggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat cctccgtgc 180
ccaatcataa aaaagtcacg accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacg 120
tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180
tctctccat cggcgtagtg gggcaccgag agggacaacc gcagccacag cgccatttc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90

gatccccgtg ccagggaccc tgcccagttc caggcgctgc ctaaccaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgacag gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgcgtg 240
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagtg ggcaccgagg aggacaaccg cagccacagc 360
gcccaattct ttgagtttct caccaaggag ctagccctgg gcc aggaccg gatacttacc 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggtcac gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcacag tgagggcctg gagataacca gctttggatt atcccgcatg caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag ctctctcatt 660
caaaaa

<210> 91

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91

gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttgagg atgattcggg 180
cacttcaggg agcttgagga taattgtoga ttttatgtga atccctgcgt aggcaatggg 240
agagggtata ataaggcagg aaaggcgag actcttcac agccatctgc aggggatggg 300
aagtccccga ccagacagag gtagatctca tttcttttg gttttcaggg atgaacctgg 360
gcttgactat ccagc ttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt 443

<210> 92

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(243)

<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92

gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaacgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctcc tgctgtgct ggggtttcaa 180
acctgctct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat 243

<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
aaacatgaac atcaaaggat cgccatggaa agggtccttc ctgctgctgc tgggtgtcaaa 60
cctgctgctg tgccagagcg tggccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccagggtgacc cttcgagacc tgtttgaccg cgccgtogtc ctgtcccaact acatccataa 180
cctctcctca gaaatgttca gcgaattcga taaacgggat acccatggcc ggggggttcat 240
taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaag acaaggagca 300
agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgatcctg 360
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgaggc 420
tatcctatcc aaagctgtag agattgagga gcaaaccaaa cggttcttag agggcatgga 480
gctgatagtc agccaggttc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tcctgaagtg 660
cogaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tggggtgaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcatgaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagtttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gctttagtag tgtcagtctg 180
actacattct tgaggcattt cacgtactct gtagtggtac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 95
gaggtcattg agaagccaga gaatcctgaa acancccaca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaagtgtc aacatggccc 120
ttaccacagc ccagccagca caaccccaga tcctcttacc acaatattac tgatgtgtgt 180
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgncctgg gttgcttgcc 360
ccaggg 366

<210> 96
<211> 2723
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2723)
<223> prolactin receptor (PRLR) gene.

<400> 96
ggaggctgaa atcccagac gccggttttc tgggctgggc tttctgctta ctcaactcctt 60
ctccctcttt ctggatttta ccgaccgttc gcgaacacagc tttccacaca atggagcttc 120
atgtctcgtg gcaggaagta ctcatcgact gatgtggcag actttgctcc ctgacaaaac 180
taaagaactc tcctattcat ggaggcgaac actgaggatg ctttocacat gaaccctgaa 240
gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
catctgcaac cgttttcaact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
tacctcctgg aaaacctgag atctttaaat gtctgtctcc caataaggaa acattcacct 420
gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
gggaaggaga gacactcatg catgaatgtc cagactacat aaccgggtggc cccaactcct 540
gccactttgg caagca gtac acctccatgt ggaggacata catcatgatg gtcaatgcca 600
ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagttc 660
agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720
acctgtggat taaatggtct ccacctacc tgattgactt aaaaactggt tggttcac gc 780
tctgtatga aattcgatta aaaccogaga aagcagctga gtgggagatc cattttgctg 840
ggcagcaaac agagtttaag attctcagcc tacatccagg acagaaatac cttgtccagg 900
ttcgtgcaa accagaccat ggatactgga gtgcatggag tccagcgacc ttcattcaga 960
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gcatctttcc gccagttcct gggccaaaaa taaaaggatt tgatgctcat ctggttgaga 1140
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ctgaccagga tacgcccctg ctgctgcccc aggagaaaac cccctttggc tccgctaaac 1800
ccttgattga tgtggagatt cacaaggatc acaaagatgg tgcattatca ttgctacca 186 0

65/292

```
aacagagaga gaacagcggc aagcccaaga agccccgggac tcctgagaac aataaggagt 1920
atgccaaagt gtccgggggc atggataaca acatcctggt gttggtgcca gatccacatg 1980
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tgggtggttt ggattacctg gatcccgcat gttttacaca ctccctttcac tgatagcttg 2160
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gctttcatga tttggcatgg gacagacgga aatgaaattg tcaaaattgt t taccataga 2520
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aaagaaaaga tgcattccag aacaaattgt ttacataagt tcctatacct tactgacaca 2700
ttgctgatat gcaagtaaga aat                                     2723
```

<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

```
gtacagttac cttttattta tagcgaatg ggggtttttc atttacagag taacaaagat 60
ttttctttaa ataatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaata caatttcnt ttgggggggg atagggngac cccctttgca 300
gagagggggt aggtgggggt tccccccggn acacacaggc aagggttttg gngccccttg 360
tgggg                                     365
```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

```
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aggggggttt gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggt 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300
```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc cttttttttn aggtttnttt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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ggagagcgcg cgctgccacc gcccacatgtc tcagccaggg ctcccttccct cggctccacc 120
ctgtggatgt aatggcggcc cctgctctgt cctggcgtct gccctcctc atcctcctcc 180
tgccctggc tacctcttgg gcatctgcag cgggtgaatgg cacttcccag ttcacatgct 240
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cttcttgcca agtccatgcc tggccggaca gacggcgggt gaaccaaacc tgtgagctgc 360
tcccgtgtag tcaagcatcc tgggcctgca acctgacct cggagcccca gattctcaga 420
aactgaccac agttgacatc gtcaccctga ggggtgctgt cctgagggg gtgcgatgga 480
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gcccctatct 540
ccctccaagt tgtccacgtg gagaccaca gatgaacat aagctgggaa atctcccaag 600
cctccacta ctttgaaga cacctggagt tcgaggcccg gacgctgtcc ccaggccaca 660
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gctgcttca caaccagggt tacttcttct tccacctccc ggatgccttg gagatagagg 1260
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aatctgccag aaacttctag cgtcagtgct ggaggagaa gctgtcagg acccaggcg 2580

67/292

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cctggagaaa gaggcctgt tactattcct ttgggatctc tgaggcctca gagtgettgg 2640
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cctgctgcat cttcccacag tggcttcaca gaccacacag agaagctgat ggggagtaaa 2760
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cctcgtctgg gtcctctgcg cctgacattc acacagagag gcagagtccc gtgcccatta 3060
ggtctggcat gccccctcct gcaaggggct caacccct a ccccgacccc tccacgtatc 3120
tttcctagga agatcacgtt gcaatggctc aaacaacatt ccaccccagc aggacagtga 3180
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tcacagtga ttgggcacct gaccacacgc cccacacagg tctgaccagc agcctatgag 3300
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ttcttaata ttttttcttt aagtcagttc attttcgttg aaatacattt ataaagaaa 3960
atctttgtta ctctgtaa at gaaaaaaccc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat 4034

```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 100

```

tttctatttt tttatatttct ttaaatgcat caaacaactg tggccagtga aaggaaacaa 60
aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggt 360
aggctccctt tgccaaaggt gggggccaaac ataattttgg cttttctggc cttcaaaaa 420
catatttccn tcgcgttttg gggg 444

```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
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acccttgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctacaaatc 120
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctggtttaac 180
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
agccacatgc tgaccacggc ccacgccgat ggcacccgcc atccagcctg tcctttggga 300
ccacaccacc cctccagctg ggtcaccgcc ntgggtttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
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acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaaccct tggaggagag 120
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgctggt 180
acctgccctc tatttattag ccaactgttt cctgctgaa tgctcgctc cttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc ttccgcttt tgaaagaagc aagacaagtt 360
ggccttggtt aggggcaagg ttagggccca ggaggccctn gggaagtttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor -related protein (PGF)
gene.

<400> 103
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tccccgggac ccgctgccc ctggcgccc cgcgcccg ggccgctccc cgtcgggttc 120
cccagccaca gccttaccta cgggctcctg actccgcaag gcttcagaa gatgctcgaa 180
ccaccggccg ggccctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240
ctctcctgt gccaggggct cccgggggga tgagcatggt ggttttcct cggagcccc 300

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ggctcgtcag aggtggaagt ggtacccttc caggaagtgt ggggcgcgag ctactgcccg 480
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```

1645

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein

ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

```

ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac

```

309

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

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papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

```
atggagaagc tgcaccagtg ttattggaaa tcaggagaac ctcagtctga cgacattgaa 60
gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
actgagggct gtggaaatga agcctgcacg aatgagtttt gtgcttcctg tccaactttt 180
cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
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cttcaagcaa aagaagactc aagaatgaa c aaagatgaa gatgaaaagg aaaaagctgc atgttctgct 600
gctgtctatgg aagaaagactc agaagcatct tcctcaagga taggtgatag ctcacaggga 660
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catacttgct ttaatgtgct ttacttccg gaatactcaa gcaaagaaaa acttaaaagag 2580
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

71/292

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106
aattttaatt ctagcacctg aagctatata agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgottaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagnccg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
ggggnggggt ttcttgaggt aggttatggt ggact gggnc caagngtggg ggggtaccacc 360
cag 363

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgcctgttgt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatatct ta tgtgggtcaaa tatttggact 180
catttaggac ttagatattt cagtgtactt gattttttta tttaactctt ttccacagcc 240
acgctaaggg taaaaggaa taatttcctt ctgtcttcct ttccaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgtttttgtt tgtaataata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108
atggccgcgg cggtggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
ggggggcggc tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgaacg 120
gattatgatc caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccggctag atatttttga tacagcagga caagaagagt t tggagccat gagagaacag 240
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gaagaaatct ataagtttca aagacagatt ctacagagtaa aggatcgtga tgagttccca 360
atgattttaa ttgtaataa agcagatctg gatcatcaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600

gtcattttct ag

6 12

<210> 109
<211> 592
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(592)
<223> 5' terminal sequence. tyrosine kinase with
immunoglobulin and epidermal growth facto r
homology domains (TIE) gene.

<400> 109
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgatgt ctggtccttt ggagtccttc ttggggagat 1 80
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccatccagcc 480
agaactnggt ctggtggccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592

<210> 110
<211> 3845
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3845)
<223> tyrosine kinase with immunoglobulin and
epidermal growth factor homology domains (TIE)
gene.

<400> 110
cgctcgtcct ggctggcctg ggtcggcctc tggagtatgg tctggcgggt gccccctttc 60
ttgctcccca tcctcttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggctcgga cgctggggc cc gccctgc tgcaggagaa ggacgacctg 240
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acgcttcgcg gcttctccaa gccctcggac ctgctgggcg tcttctcctg cgtgggcggt 360
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ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacacctg 540
gactggcatg aagcccagga tgggcgggtc ctgctgcagc tcccaaatgt gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc ccctgggcag cg ccttcttt 660
cggctcatcg tgcggggttg tgggctggg cgctggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcactg gcacccgctg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

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caggagcagt gccagagcat atcaggctgc cggggcctca ccttctgcct ccagacccc 900
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ggtcattttg gggctgattg ccgactccag tgccagtgtc agaattggtg cacttgtgac 1020
cggttcagtg gttgtgtctg cccctctggg tggcatggag tgcactgtga gaagtcagac 1080
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cggatcaact gtgcagctgc aggaacccc ttccccgtgc ggggcagcat agagctacgc 1200
aagccagacg gcactgtgct cctgtccacc aaggccattg tggagccaga gaagaccaca 1260
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cccttggtcg caccctggct cctgaccaag cagagccgcc agcttgtggt ctccccgctg 1440
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aaccgaggtt acttgtatat cgtattgaa tatgccccct acgggaacct gctagatatt 2 820
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384 5

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(202)
<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111
aaagcccttc aaggtttact cncccanctt gcaaggccca cancttggtc aaggaccaa 60
cccacaggct ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
acccatgggg canantnatg ag 202

<210> 112
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(450)
<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112
attcaagtac cttttoctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgaggt ggaagtggag 180
cccagtgagg tgaagactt cgaggctcgt gggagcgctt tctccaagtc tgctgatgag 240
agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ctttcggaaa 360
ggtgccgttc cttttgaacc ccgtgaaccc ctgncgttcg aaaggattgc ttggcttgcc 420
cgccgcggga aacggaggct ttcagaagca 450

<210> 113
<211> 1810
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1810)
<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113
ggggggaagg ccaagcagtg accaggaaga gggagaaact tctgctcaga ccgagcgtgt 60
gccactggac ctacgtcctc gcctggagga gacgtggac ttcggcgagg tggaagtgga 120
gcccagtgag gtggaagact tcgaggctcg tgggagccgc ttctccaagt ctgctgatga 180
gagacagcgc atgctggctg cagcgtaagg acgaactcct ccagcaagct cgcaaactgt 240
tcttgaacaa aagttctgaa gatgatgcgg cctcagagag cttcctcccc tcggaagggtg 300
cgtcctctga ccccgtagac ctgctgagaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgctccct tgccttctc agctgcct cc tgcgccctgt 420
gcccgactga ctggaggagg cctgtcccaa ttctgccgct ccatggaaaa ggggcttga 480

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ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
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taactgtagg tatgatctct tctggg gttg actggactgc ttgggggtggg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
gtcccacaaa tgcaggtgtc ctgagcacca caccagctgg gaagagtgtg ggggaggcgc 780
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cggaaagttt ttagaatgtt gaaaagtaat tgaaaagggt gataggtaaa tttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaat 1740
tctgtgcatt ttttttttt aatttgttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc 1810

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<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST
 R81127) gene.

<400> 114

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gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtntccn acttttacia tgtgtacaat gtttcacat gtnccaatta atggttgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt 248

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<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
 (BCL2) gene.

<400> 115
ttttttaag cagctttoga aatatcaacc acagcattaa acattgaaca ggtacattc 60
caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt cccaccatt gattttnttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accggggnac ttttttttg tcagggtttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattcn tgggcccggg 360
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<210> 116
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 116
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attgtgtata ttcatatatt ttggatacgc acccccacac tcccataact ggctctgtct 120
gagtaagaaa cagaatcctc tggaaactga ggaagtgaac atttcggtga cttccgcac 180
aggaaggcta gagttacca gagcatcagg ccgccacaag tgcttgctt t aggagaccg 240
aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtcttgaggaa ctgagccggg 300
gccctcactn gcctcctcca gggatgatca acaggngcag tgtggtntcc gaatgtctg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaa agncagtaga ggggtgtngc 420
tgggncctgtt cacctggggg ccctncaggt agngcccntt tttcacgt 468

<210> 117
<211> 6030
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6030)
<223> b-cell cl1/lymphoma 2 (BCL2) gene.

<400> 117
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taaccgggag atagtgatga agtacatcca ttataagctg tcgcagagg gctacgagt 120
ggatgcggga gatgtgggag ccgcgcccc gggggccgccc ccgcgcccgg gcatcttctc 180
ctcgcagccc gggcacacgc cccatacagc cgcattcccgg gaccg gtcg ccaggacctc 240
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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

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<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
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oncogene homolog) (ERBB2) gene.

<400> 119

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<210> 120

<211> 319

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

<400> 120

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<210> 121

<211> 2372

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

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<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 122
atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60
gacagggcga ngaggcagcc nggcccataa ncaggacgtg gccnntcggc cagggttcgc 120
tgacatgcac gctggtagct catacactgc taccctcagc acaggctgca ggaataggga 180
caagacagat gccgccggac tcttaggaag ctatttaata aatatcatcc aaanacaaaa 240
tgggaaaaag aaacaaggaa accctccggg gcacaaccac cttagggggc aactggaatg 300
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 123
cgagttagnt atgttgagg aacatgttgt gtctgccgtt tttgaatacc cagggtggga 60
gcttgccat ctgcatcccc acttoccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaataa caattctcta cgttcactgt tcccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 124
gccagggctc agtgggcaag ggctctgtgc cgtngnccgtg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcatcgagg tgatcgacga 120
aggctgggtg cgtggctatg ggccggatca tntgttngca tgttccctgc caactacgtg 180
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ccccagttga ggattgaggc ntcagggttc cctccggnnt gggcagattc agccttttca 360
ccccaaatgg cagcaattgg cntgggtgat tccccacaaa tcnttcctg cattcccccg 420
acctttccca gacagtttg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain-containing protein
hip-55 (HIP-55) gene.

<400> 125

```
atggcggcga acctgagccg gaacgggcca gcgctgcaag aggcctacgt gcgggtggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgcggtggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gacccaact ctggactgcc caaatattgtc 240
ctcatcaact ggacaggcga gggcggtgaac gatgtgcga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gcccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcttcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcag gacgtgggac cccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttctgg 540
gccaaagcag agaaggagga ggagaaccgt cggtggagg aaaagcggcg ggccgaggag 600
gcacagcggc agctggagca ggagcgccgg gagcgtgagc tgcgtgaggc tgcacgccgg 660
gagcagcgct atcaggagca gggtggcgag gccagcccc agaggacgtg ggagcagcag 720
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ccagctgtg ccatctcaag gcccagggca gatctccctg ctgaggagcc ggcgcccagc 960
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gaccaccaca ttcagggccca ggggtcaggt gggcaagggc tctgtgccc tgccctgtac 1140
gactaccagg cagccgacga cacagagatc tcctttgacc ccgagaacct catcacgggc 1200
atcgaggtga tcgacgaagg ctggtggcgt ggctatgggc cggatggcca ttttggcatg 1260
ttccctgcc actacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag cccaatccc aacccacct ccaggccaat acatgccctc 120
gggactggct cagtccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tactccttc cagctcatcc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggggtggga gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gagggneccg gaggacggcc ttgggtnttg g ggtaagggc 360
ttaanccagt cngggctttg gtaagggcc gnaagggat tccntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(339)
<223> 5' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 127
gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
acatgatccc ctgtgagaag gtgtccacc c tgcccgcgat cacactgaag ctgggaggca 120
aaggctacaa gctgtcccca gaggactaca cgctcaaggt gtcgcaggcc gggaagaccc 180
tctgcctgag cggttcatg ggcattgaca tcccgcacc cagcggncac tctggatcct 240
ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300
tgggtttcgc gaggttgcc cgcttttagt ttcccaagg 339

<210> 128
<211> 1988
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1988)
<223> cathepsin d (lysosomal aspartyl protease)
(CTSD) gene.

<400> 128
ccatgcagcc ctccagcctt ctgccgctcg cctctgcct gctggctgca cccgcctccg 60
cgctcgtcag gatcccgctg cacaagttca cgtccatccg cggaccatg tcggaggttg 120
ggggctctgt ggaggacctg attgccaaag gcccgcgtctc aaagtactcc caggcgtgct 180
cagccgtgac cgaggggccc attcccaggg tgctcaagaa ctacatggac gccagttact 240
acggggagat tggcatcggg acgccccccc agtgcttcac agtcgtcttc gacacgggct 300
cctccaacct gtgggtcccc tccatccact gcaaaactgt ggacatcgct tgctggatcc 360
accacaagta caacagcgac aagtccagca cctacgttaa gaatggtacc tcgtttgaca 420
tccactatgg ctcgggcagc ctctccgggt acctgagcca ggacactgtg tcggtgccct 480
gccagtacg gtctgcagcc tctgccctgg gcggtgtcaa agtggagagg caggtctttg 540
gggaggccac caagcagcca ggcatcacct tcatcgagc caagttcgat ggcacccctg 600
gcatggccta cccccgcac tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
agcagaagct ggtggaccag aacatcttct ccttctacct gagcaggac ccagatgcgc 720
agcctggggg tgagctgatg ctgggtggca cagactccaa gtattacaag ggttctctgt 780
cctacctgaa tgtcaccgac aaggcctact ggcaggtcca cctggaccag gtggaggtgg 840
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ggaggtgggg ttgggattgg gggctggtgc cagccttcct ctgcagctga cctctgttgt 1920
cctccccttg ggcggctgag agcccagct gacatggaaa tacagtgtgt ggctccggc 1980
ctcccctc 1988

<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin -like growth
factor 1 receptor (IGF1R) gene.

<400> 129

gtggcggcac tcattgttct cgggtgcacgc ccgcttccca cagtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atggtccctg gacacaggtc cccacattcc tttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tcctgatggc cccccgagta atgttctca 300
ggttgtaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggttnttg gaaggagntt ttcca 385

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor
(IGF1R) gene.

<400> 130

ttttttttt ttttgagaaa gggaatttca tccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt ccccgacctc gctgtggggg ctctgttct tctccggcgc gctctogctc 120
tggccgacga gtgga gaaat ctgcggggcca ggcacgaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacgggtgatc gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctccggagacc tcttcccaa cctcagc gtc 360
atccgcggct ggaaactctt ctacaactac gccctggtca tcttcgagat gaccaatctc 420
aaggatattg ggctttacaa cctgaggaaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactggtccc tgatcctgga tgcggtgtcc 540
aataactaca ttgtggggaa taagcccca aagga atgtg gggacctgtg tccagggacc 600

atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
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 gagaacaatg agtgctgcca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
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87/292

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gactgcccct gctgtgtgc tcaaggccac aggcacacag gtctcattg c ttctgactag 4920
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tgaaccggc 4989

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<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

```

gggcaacaat ctggcagctg agctagaagc caacctcggc ctcatgaag aaatttcagg 60
gtatctaaaa atccgccgat cctacgctct ggtgtcactt tcttcc ttcc ggaagttacg 120
tctgattcga ggagagacct tggaattng gaactactcc ttctatgcct tggacaacca 180
gaacctaaag cagctctggg actggagcaa acacaacctc accatcactc aggggaaact 240
cttcttccac tataaccoca aactctgctt gtcagaaatc cacaagatgg gaaggaaagt 300
tcagggaacc aaggggncgc cagg aggaga aacgacattt nccctggaag gaccaatggg 360
gggaccaggg catcctgtgg aaaaatggag tttactttaa anttttgctt taacattngg 420
gacntttttt tggacaagtt ttttgttgaa gttggggagc cctnattttg 470

```

<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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ccggcggggg gcggcgccg cgccgtgct ggtggcggtg gccgcgtgc tactggggcg 180
cgcgggccac ctgtacccc gagaggtgtg tcccgcatg gatatccga acaacctcac 240
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gttcaaaacg agggccgaag att tccgaga cctcagtttc cccaaactca tcatgatcac 360
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```

cctcacggtc atccggggat cagcactgtt ctttaactac gcgctggcca tcttcgagat 480
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 catcgagaag aacaatgagc tctgttactt ggccactatc gactgggtccc gtatcctgga 600
 ttccgtggag gataatcaca tcgtgttgaa caaagatgac aacgaggagt gtggagacat 660
 ctgtccgggt accgcgaagg gcaagaccaa ctgccccgcc accgtcatca acgggcagtt 720
 tgtcgaacga tgttgactc atagtcaactg ccagaaagtt tgc ccgacca tctgtaagtc 780
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<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

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<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

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<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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94/292

```

agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
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tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccacccca 5340
tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
cacacacaca tacaaaatgt tccttttgct tttaaagtaa tttttgactc ccagatcagt 5460
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```

<210> 138

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 138

```

ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtgc aaagtgtgcc 60
tacagtatac aaggtaaact cacaactcat caaaactaaa actttttaca atgtgcaata 120
catgtaggga tattaattca atatataaat gtcacatgtc tcccaaatgt caccaggct 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttata ctaactttat gtatacttct ctaaagattc ttagggcttg taagcaatga 300
ggtttaaggc natttttttag gatggttagca tcccggggct gacttngccg ggctgtggga 360
acccaggnc cgagtggtg 378

```

<210> 139

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 139

```

gctttcactg gcatgggaga cccttgacac ctgctgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtatgccca 120
tgcatggatc tatgtagtat gctctgactc taataggact gtatatactg ttttaagaat 180
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ggatattttg atatttacct ttatgttga atgctattaa atgttttccn gtgtccaaag 360
taaaatattg ttttaataaac ctaacaatgg accccgatag tacag ggta agtgagggga 420
accttatgga ttctaacaag tcctagg 447

```

<210> 140

95/292

<211> 4138

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4138)

<223> tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) (TEK) gene.

<400> 140

```
cttctgtgct gttccttctt gcctctaact tgtaacaag acgtactagg acgatgctaa 60
tggaagtc caaaccgctg ggtttttgaa aggatccttg ggacctcatg cac atttgtg 120
gaaactggat ggagagattt ggggaagcat ggactcttta gccagcttag ttctctgtgg 180
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gctggaagtt actcaagatg tgaccagaga atgggctaaa aaagttgttt ggaagagaga 420
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caggatacga accatgaaga tgcgtcaaca agcttcttct ctaccagcta ctttaactat 540
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agatgcagtg atttacaaaa atggttctct catccattca gtgccccggc atgaagtacc 660
tgatattcta gaagtacacc tgcctcatgc tcagccccag gatgctggag tgtactcggc 720
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tgaagccag aagtggggac ctgaatgcaa catctctgt actgcttgta tgaacaatgg 840
tgtctgccat gaagatactg gagaatgcat ttgcccctct gggtttatgg gaaggacgtg 900
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96/292

```

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```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

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taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca tttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaattctta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcaggtttt acatggggac 300
attattgaac atttctgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggtt angacatgtt caca 395

```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

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tcgtaattgg catcaacttc atggaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatctttgta ctcttcgag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgcac tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
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gccacatat ttgtaggttt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagttagg ggaacaacac ttcttcaag ggttaaagtc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggtt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

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gtgacttggc tggagcctca gggcggggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccga ggcgagctg cctcttctcc cgcgggttgg tggaccctgt cagtacggag 180
ttggggaagc tctttcactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgctc aaaagtgtta atgccccagt 300
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gaacttggaa gccttgcatc atgatggcca attctgccat aagccctgtc ctccaggtga 420
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tgatgaagga catggccttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
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caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaga 720
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aattataatg tttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
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```

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ggaaccacct aaagaacttc catttatgga ggattttttt gcccttctgtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

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gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tggaagaaac ggaaccagga cacatgggga gccgagagaa aacagtccag gccagtatgt 180
tacaggagct ggaaggtnnt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcacaac gttagtcca ggaagacaa ctactcccag ccccatatga 300
gcccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttccgct ggctaattca aagtgcaatg aactggggag ggatgggggtg gatgaggaag 420
gttcgntgga cgtt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

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cttgtgctgc ntncagggga gcaggctgaa gggccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcgcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctcaaga ggaagcccta atccgccac aggaagcctg cagtccctga agcgcgaggg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttccgccagg caccgaggca 60
ctcagaggag gcgccatgtc agaaccggct ggggatgtcc gtcagaacct atgcggcagc 120
aaggcctgcc gcgcctctt cggccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttcgcttg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaag accatgtgga cctgtcactg 420
tcttgtacc ttgtgcctcg ctcaggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcgcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgcccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tcctcatgta cataccctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta acaaaaaact aggcgggttg atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcacccctg 840
ttctcctttt cctctctccc ggaggttggg tgggcgggct tcacgccagc tacttctccc 900
tccccacttg tccgctgggt ggtaccctct ggaggggtgt ggtccttccc catcgctgtc 960
acaggcgggt atgaaattca ccccttttcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaagg gcctcacoga gtgggggcat catcaaaaac 1080
tttgagtgcc cctcacctcc tctaagggtg gcaggggtga ccctgaagtg agcacagcct 1140
agggctgagc tggggacctg gtaccctcct ggtctttgat acccccctct gtcttgtgaa 1200
ggcaggggga aggtggggtg ctggagcaga ccaccccgcc tgcctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc ccctgtacct 1320
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gggcacccta gttctacctc aggcagctca agcagcgacc gcccctcct ctagtgtgg 1560
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gtatatgatg ggggagtaga tctttctagg agggagacac tggccctca aatcgtccag 1680
cgaccttct catcaacccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcag acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
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taacatactg gcctggactg tttctctctg gctcccatg tgtcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacacc tgtactgttc tgtgtctttc 2040
acagctcctc ccacaatgct gaataacag caggtgtcca ataatgatt cttagtgtgact 2100
ttaaaaaaaa aaaaaaaaaa a 2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac ccccgaggat acagcttctt tggtaaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtctct tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctcctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggg gaatttccac agaatgatca agttgacgac aggaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgacag aggatcccc aaggatgcaa 300
cggattcgct gctgtg tcac tcatgactgt ttgtctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttacatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccac atttctgagc tacaagttta gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgctga gtccccctctt ccctggaaac cttccacca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag ccctctctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854

<210> 150
<211> 224
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> misc_feature
<222> (1) .. (224)
<223> 3' terminal sequence.
glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150
ggttgagcac agggactttt attgatgna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggaggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagtggg ggtctctctc ttcctcttnt gctcttntctg 180
gggntggtgg nccagggnntn ttactccttg gaggccatnt gggc 224

<210> 151
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> misc_feature
<222> (1) .. (359)
<223> 5' terminal sequence.
glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151
gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatc tctctgcccc ctctgctgat gcccccatgt 120
tcgtcatggg tgtgaacctt gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcacccctgg gccagggtca tccatgacaa ctttggatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctnccggg aactgtgggc gtgatggccg cgggggttctt tcagaacatc atccctgcc 359

<210> 152
<211> 1283
<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttcg acagtcagcc gcatcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtccgagtcac acggatttgg tcgtattggg 120
cgccctggta ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccacatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgcc ccatgttcgt catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcattg 600
accacagtcc atgccatcac tgccaccag aagactgtgg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagtgaac gggaagtcca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggt gaagcaggcg tcggagggcc ccctcaaggg catcctgggc 900
tacactgagc accaggtggt ctctctgac ttcaacagcg acaccactc ctccacctt 960
gacgctggg cttggcattgc cctcaacgac cactttgtca agctcatttc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtggtg gacctcatgg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagtgtg 1200
ccatgtagac cccttgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc 1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence.

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcgggcttga gta ccaggcg gcggggccag 180
ctccntant ncgccccctc ttccctccc tgttaaatac acaaataat tatattcaat 240
ntgaatcng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcgangg ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t 361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaaggtga agacgctcaa ggccgagaac 120
gcgggngtgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagcaa cggctntnag ctgctgcttn gggtaaggag acacgccttc 240
tggaacgttc cctgcccttc tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttccactn gggttccagg gttagcaggcg gtggggnacc cacctggggg acntaggggg 360
cgnccgcaaa ccacattngg atttcgggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto -oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggct tttgcgcaca gctgccggct ggctgctacc 120
cgcccgcgcc agcccccgag aacgcgcgac caggcaccca gtccggtcac cgcagcggag 180
agctcgccgc tcgctgcagc gaggcccgga gcggcccgcc agggaccctc cccagaccgc 240
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctgggtg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcggtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420
cggacccgcc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgctct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgatgc acgacgacgc ctacaccccc gggacagtac ttttaccccc gcgggggtgg 600
cagcggtgga ggtgcagggg gcgcaggggg cggcgtcacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg gcgctaccg gggggccccc ggtggggccc gggggcgct acgccggccc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgccggg gctgcccgtc ggaccgggag ctctgaccgg acgaccacca tcagctacct 900
cccacacgcg ccgcccttgc ccggtggcca cccggcgag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt cccggaggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tggaagacca agagcgcatc aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgcca ccaagtgcg gaagcgggag ctggagcgca t cgcgcgcct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcggg ctgtcgagta ccgccggcct 1200
cctccgggag cagggtggccc agctcaaaaca gaaggtcatg acccagctca gcaacggctg 1260
tcagctgctg cttgggggtca agggacacgc cttctgaacg tcccctgccc ctttacggac 1320
accccctgc ttggacgggt gggcac acgc ctcccactgg ggtccaggga gcaggcgggtg 1380
ggcaccaccc ctgggaccta ggggcgcgcg aaaccacact ggactccggc cccctaccc 1440

104/292

tgcgccagct ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500
 tttttttctg ctggaaacag actcgattca tattgaatat aatatatttg tgtatttaac 1560
 agggagggga agagggggcg atcgcgccgg agctggcccc gccgcctggt actcaagccc 1620
 gcggggacat tggaagggg acccccgcgc cctgccctcc cctctctgca ccgtactgtg 1680
 gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
 gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
 acid-binding protein 2 (CRABP2) gene.

<400> 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60
 ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcctctt tagagagacc 120
 ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccggg 180
 aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
 ggtcaaagaa agcaagaccc tgcaagaggc atccagtgga cccccagaag tgactggggg 300
 aaggggagcg ctatcctagg anggtggggg tgggt 335

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
 acid-binding protein 2 (CRABP2) gene.

<400> 157

gcctggactt gtcttgggtt ccagaacctg acgaccggc gacgcgacgt ctct ttgac 60
 taaaagacag tgtccagtgc tccagcctag gactctacgg ggaccgcctc ccgcgccgcc 120
 accatgccca acttctcttg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
 ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
 ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300
 cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
 gggaggccct gttaaggagc nggggtgaaat ggggagagtg aggattaaat ggtcttttga 420
 gcagaagttc ctgaagggng aggggcccga agacntcttg gaccngagaa tttccccacg 480
 t 481

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaag 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tgggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aagggagagg gccccaagac ctcgtaggac agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accaggggtc 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgcctg cttcactgcc cct ccgtcc caccocctcc ttctaggata gcgtcccct 660
taccocagtc acttctgggg gtactgga tgctcttgc aggtcttgc tttctttgac 720
ctctctctc ctccctaca ccaacaaaga ggaatggctg caagagccca gatcaccat 780
tccgggttca ctcccgct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctt aaaggggact tgagggcctg agcaggaaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa                                     969
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcgnttga ggggaggtg ccccgntcc gccgangaan tgcgcccg cc acccgagag 60
cncncagagg gaccattgac cttgggctcc cccaggaaaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga cctgtgaag cgtctcggg gccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccggggg cctgggtgca cagtagtgct 240
tgggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
aggagantct tgcagggggg gcgcccacc gatttcgttc aacc                                     344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcatc cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccccc acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccagggaa ggggagccct gagccactcc 180
ctgtgggtgg cagtcaactgt ccaggagggt cccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaacacgggt ttattaggag ggagtgggtg agctggggcca ggcaggaaga cgctggaata 60
agaaacatctt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcgagccc ctcccgggt ccagcccgggt ccggggccgc gccggaccc c agcccggcgt 180
ccagcgctgg cggtgcaact gcggcgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggctagcgc ccgcccacce gcagagcggg ccagaggga ccatgacctt gggctcccc 300
aggaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctggtgac ctgcaog tgt gagagcccac attgcaaggg gcctacctgc 420
cggggggcct ggtgcacagt agtgcgtggt cgggaggagg ggaggcacc ccaggaacat 480
cggggctgcg ggaacttgca cagggagctc tgcagggggc gccccaccga gttcgtcaac 540
cactactgct gcgacagcca cctctgcaac cacaactgt ccttggtgct ggaggccacc 600
caacctcctt cggagcagcc gggaacagat gccagctgg cctgctcct gggccccgtg 660
ctggccttgc tggccctggt ggccctgggt gtccctgggc tgtggcatgt ccgacggagg 720
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
tctgagcagg gcgacacgat gttgggggac ctccctggaca gtgactg cac cacagggagt 840
ggctcagggc tccccttccct ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960
gccgtcaaga tcttctctc gagggatgaa cagtctggt tccgggagac tgagatctat 1020
aacacagtat tgctcagaca cgac aacatc ctaggcttca tgcctcaga catgacctcc 1080
cgcaactcga gcaogcagct gtggtcatc acgcactacc acgagcacgg ctccctctac 1140
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gcatcgggcc tggcgacact gcacgtggag atcttcggt caccagggcaa accagccatt 1260
gcccaccgag acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcatc 1320
gccgacctgg gcctggctgt gatgactca cagggcagcg attacctgga catcggaac 1380
aaccgagag tgggaccaa gcggtacatg gcaccgag tgctggacga gcagatccgc 1440
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cagaccccca ccatccctaa ccggtggct gcagaccggt tccctctcagg cctagctcag 1680
atgatgcggg agtgctggtg cccaaacccc tctgcccagc tcaccgcgct gcggtcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
 ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
 tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162
 <211> 407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(407)
 <223> 5' terminal sequence. lim domain protein
 (RIL) gene.

<400> 162
 gtgaccctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
 cgccccac catctcagcg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
 caggagacct gatccaggcc atcaatggtg agagcacaga gtcctgac a cacctggang 180
 cacagaaccg catcaaggcg tgccacgac acctcacact gtctgtgagc aggcctgagg 240
 gcaggagctg gccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
 ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360
 gggccagaag atnngcagan caagnct ggg gtttttncat atggaca 407

<210> 163
 <211> 1130
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1130)
 <223> lim domain protein (RIL) gene.

<400> 163
 tgagagtccg gctcaggctc cggtgcggc tccagcccgc gatgcccac tccgtgacc 60
 tgccgcccc ttccgctgg ggcttccgcc tgggtggccg ggacttcagc gcgccccca 120
 ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
 tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
 gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
 ggcccagtcg cctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
 tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
 atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
 atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
 ccagcgctga ccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600
 aggtgtacag gatgctgcgg gagccggccg agcccgtggc cgcggagccc aagcagtcag 660
 gctccttccg ctacttgacg ggcattgctag aggcggcgga gggcggggat tggcccgggc 720
 ctggcggccc ccggaacctc aagccacagg ccagcaagct gggcgctccg ctgagcggcc 780
 tgcaagggct cccgagtgac acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
 aacgggacaa gctctacat cccgagtgct tcatgtgcag tgact gcggc ctgaacctca 900
 agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
 gcgtgaagcc gcccgaggcg tacgacgtgg tggcggtgta cccaatgcc aaggtggaac 1020
 tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cgcccggtgt 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctgtc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

anattcgga caggggatcc ctctatgtc aacgtccaga acctagacaa ggcccggcaa 60
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agccttcga agatgctctt cgctgc ctc caccctccca gtcggtgtcc 180
atgntgagc agtccgagg ggagccctgg gttccatggg aagctgagcc ggccggaggc 240
tgaggcactg ctggcagctt caatggggat ttccnggtac gggagagcac gaccacacng 300
gggcaatatg 310

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain -containing) transforming protein 1 (SHC1) gene.

<400> 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggtaagg gcctggggat 120
accctctgcc tggccccctt gccaaaactg gcaggggggc caggctgggc agcagccccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgtggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
ccccatcagc ttcateccctg gggcccatcc tgctctctct gcctggggac gatagtccca 360
ctaccctgtg ctctttcttc ccccgatga gcaacctgag gctggccaac ccggtgggg 420
ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
gggcagccat gccagagtca ggccccctac ccctcctcca ggacatgaac aagctgagtg 540
gaggcggcgg gcgcaggact cgggtggaag ggggccagct tgggggcgag gaggggaccc 600
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcacccaac gacaaagtca 660
tgggaccggg ggtttcctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720
tgctgcccct ggacttcaac acccgactc aggtcaccag ggaggccatc agtctggtgt 780
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
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tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gccaacccacc 960
acatgcaatc tatctcattt gcacccggcg gggatccgga cacagccgag tatgtgcctt 1020
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtggt cccgaagggc 1080
ttgcccagga tgtcatcagc accattg gcc aggccttcga gttgcgcttc aaacaataacc 1140

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ctgctcgacc cactgcaccc aatgccaga ccccagcca cttgggagct acattgcctg 1380
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cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
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tggacctga ggggtgtggt cggactaagg atcacgctt tgaaagtgtc agtcacctta 1860
tcagctacca catggacaat cacttgcccc tcatctctgc gggcagcgaa ctgtgtctac 1920
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aatgatattt tatgcaaaca gttcttggac ccctgaattc ttcaatgaca gggatgccaa 2460
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actctcccag gtgatt ttg tggagtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccc cataccatct gtgagtttg aactgcattc ttttaaagtt ttatatgcat 2940
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caaaatgata atcaattatt acattttatac atcacctttt tgacttttcc aagccc tttt 3060
acagctcttg gcattttcct cgctaggcc tgtgaggtaa ctgggatcgc accttttata 3120
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gccacaccac agcaagccgg cccccctct tttggccttg tggataagg agagtggacc 3360
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gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt 3480
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ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664
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<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

110/292

```
gagcacaggg tncctttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggt cttac tccttgagg ccattgtggc atgagggtcca ccacctgtt 240
gctgtagcca aattcgttgt cataccaggg aatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagccttc gaagggtgag gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccaggga tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
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<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

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tggttcagacg tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggtcg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tgttgccatc aatgacctt ctttgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttcaaccac ctttgagaa gggtttggg gttcatttn 420
caaggggggg gagcccaaan ggtcttcat tttttggccc ccttttt 467
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<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

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ggcttggtgtt tntntctctt ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggcgc cctcccacc agcctgagac cgctctctgc ctctctctc 120
tcctctcttc tccagcatct cac ccacttt ctctccttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtccacc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagntccac aggggctagt 300
cccctgggnt acctgc 316
```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

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atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacgggtga tgatcaagac catcgagaca cgggatgggg 120
aggctcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgtccct gaagccagcc ttcttccatc 240
ccagggacac cacaccca gc cttcagtct ccccttcaca gcctctggac ccctcctcac 300
tgggccattc cctcgtggtt cccaacagc ggacataggc ccctccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgctgg aacccagtt gttgaggctt tgggtgtttg 420
ggcagttgag ttgaggcttt                                     440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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cctcgccgca tccactctcc ggccggccgc ctgccgcgc cctcctcc gt gcgccgccca 60
gcctcgcccg cgcgctcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcccgcac ctccggcggc gccccgggct tcccgcctcg ctccccgctg agctcgcccg 180
tgttcccgcg ggccgggtttc ggtcttaagg gctcctccag ctccgtgacg tcccgcgtgt 240
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tggggaccac ccgcacgccc tctcctacg gcgcaggcga gctgtggac ttctacttg 360
ccgacgcggt gaaccaggag ttcttgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtgcg cttcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccaaagtgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tggtgacgac tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcattgag aggagatccg tgagttgcag gctcagcttc 840
aggaacagca ggtccagggt gagatggaca tgtctaagcc agacctcact gccgcctca 900
gggatatccg ggctcagtat gagac catcg cggctaagaa ctttctgaa gctgaggagt 960
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gccaggccaa gcaggagatg atggaatacc gacaccagat ccagtcctac acctgcgaga 1080
ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
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aaaggggttc tgaggtccat accaagaaga cggatgatga caagaccatc gagacacggg 1440
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ccctctgcca ccagagaccg tctcaccgcc tgtcctcact gctccctgaa gccagcctt 1560
```

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cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgacccctcc 1620
tcactggcca tccctcgtgg tccccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagttag 1740
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gtctcttact ttctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
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tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
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<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

gatccacgac cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttgggttactg tcctcgtgtg tactgtgaga accagccaat gcttccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccga gtgcatggat 180
gtgtacacac ccaagtcac cagacacat cagacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggcccaaggg gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncggtgggg cttaccagg 360
tgcaggt 367

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

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tgcgcggtgc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact cegtgtccc gcatccaccg cggcacctga ccttgggcgc ttgcgtgttg 180
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ggtccgcggc ctgcgctgta gcgg tcgccc cegtccctg gaagtagcaa ctccctacc 300
ccacccagc cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggagg 360
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agactacatc caggacaaat ttaattctac tggactcaat gagcaggctc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

```
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cccagtgtaa gccatggtga agctctactg ccccaagtgc atggatgtgt acacacccaa 780
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caagagccca gtcaagacga ttcgctgatt cctccccc cctgtcctgc agtctttgtc 1020
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<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

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acaaaggcag taaccccagc gaccagctgc tgctgtgca cggtagaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggttnagtgg ggaatnctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggtaaggt gggctctacc 360
ccgtccnttg agctctngtg tncactncgc ttgggggata cctcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475
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<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

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ggtcatctct tgcctgaagc tgagatatgc tgaccagcgc ctgtcttcag actgtgaaga 60
ccagatccga atcattatcc aggagtccgc cctggactac cgcctggatc ctacagctcca 120
gctgactgca tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgacccggt 300
acttcatact tgcttggtgc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat gggaaggcac tgggagggtt aaggcgggtt 420
gaggtttaca gcccgaagtt caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483
```

<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
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ccaggcgctc ccacagccag ggccagggtc ccggggccaa ctttgtgtcc ttcgtagggc 180
aggccggagg cggcgggccc ggcgggtcagc agctgcccc a gctgcctcag tcatcgcagc 240
ttcagcagca tagcagcagc cagcaacagc aacagcagcc tcagccgccg cagccgcctt 300
tcccgcgggg tggcctccg cgccgggggag gagcgggggc tgggtggggc tggaag ctgg 360
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acaacctggc ggtgctcgag tgcttcgagg atgtgaggga gcctgaaaat gaaatttctt 480
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aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600
aaccggttgg aaaagggttac atggttttct gcttagtgga tcaccgaggc aacatcactg 660
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aagccattct ccgggtggct gagctgtcat cggatgactt tcaactagac cggcatttat 960
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cagcctgcaa acatataaga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620
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cagagctaga ctacaccctc atgaggggtct gcaagcagat gataaagagg ttctgtccgg 2700

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aagcagattc taaaaccatg ttgcagtgt tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaagt caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaccccat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggtatcc 2880
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tgcccttggt tggcaaacct ggggttacct gcctgtagac aagtct ctct cataccaaca 3840
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aaaccacca
3909

```

<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

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gttaagatca aacctcaca agagaaatag aatgtttgaa aggctatccc aaaagacttt 60
tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaatct tcttctttca ctatcgtagc tttaaactctg tttggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaa 360
gggtttctag gcatatgtat tatggctatt
390

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<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 aggtaggcat ttgcccgggt gggacgcctt gccagagcag tgtgtggcag gccccctgg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgcgccctg 300
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 ccacgcacca tctccctcc cccgtgccaa ggacccatcg agatcaagga gactttcaaa 540
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 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
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 ctgctggcag aggactggcc atttggagct gagatgtgta agctggtgcc tttcatacag 780
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 gccaaaaccg tcttttgcct ggtccttgtc ttgtccc tct gctggcttcc cttcacctc 1260
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 gaaagaaaga gcaataataa ttaattcaca caccataggt attctattta taaatcacc 3360
 acaacttgt tctttaattt catcccaatc actttttcag aggcctgtta tcatagaagt 3420
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 tcttgatacc ctttcttctt ccatgtcagt atcatgttct ctaattatct tgccaaattt 3600
 tgaaactaca cacaa aaagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

117/292

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtag taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgta 3840
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tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttattttttc 4140
actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataaatgtga 4200
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<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtcctgc aaccccgact gccaccctcct tgggaattct 60
tgcctctgtc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnntcat tgttctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ccagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
ttctgcactn ttcaggaaca atttcctgaa gtgtgggttg ctaaagtgtc cattgagaaa 420
taacccagc ccaggccaaa ttgaaaagtt gcctgggntt tt 462

```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

```

agcagctcca accagggcag ccttctgag aagatgcaac caatcctgct tctgctggcc 60
ttctctctgc tgcccagggc agatgcagg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
ggtggcttcc tgatacaaga cgacttcgtg ctgacagctg ctcactgttg gggaagctcc 240
ataaatgtca ccttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gacccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

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118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca agggccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggag 480
acggccccc tgggaaaaca ct cacaacaca ctacaagagg tgaagatgac agtgcaggaa 540
gatcgaaagt gcgaatctga cttacgccat tattacgaca gtaccattga gttgtgcgtg 600
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tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
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agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 180

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aaaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
ttttttcttt ttgtttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
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caggggccan caacactgcc cccaacctgg gccttcgcct caccatcctc tgggtaccgg 360
gcntttgggt caggcaaaagc aaactagtnt cgggtttatt angccactgg naccaccttt 420
ttgggggcag aggtcacctt cattcgaggg cacgangcac tgacctcctt t 471

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

gctttgtgc cagccacttc atccccctcc agatgttggg ccaacacccc tccctgccac 60
caggactgcc tggaggagg agtgggagcc aatgaacagg catgcaagt agagcttct 120
gagctttctc ctgtcgggtt ggtctgtttt gccttcaccc ataagcccct cgactntgg 180
tggcaggtgc cttgtcctca gggctacagc agtagggagg tcagtgttc gtgcctgat 240
tgaaggtgac ctctgcccc gataggtggg gccagtggct ttattaat tc cgatactagt 300
ttgctttgct gaccaaagtc ctgggtacca gaggatggg aggcgaaggc aggttggggg 360
cagtgttgtg gccngggggc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

cctcttgcgg ccacaggcgc ggcgtcctcg gcggcgggcg gcagctagcg ggagccggga 60
cgccgggtgca gccgcagcgc gcggaggaac ccgggtgtgc cgggagctgg gcggccacgt 120
ccggacggga ccgagacccc tcgtagcgca ttgcggcgac ctgccttcc ccggccgcga 180
gcgcgccgct gcttgaagg ccgcggaacc caa ggacttt tctccggtcc gagctcgggg 240
cgccccgcag gcgcacggta cccgtgctgc agtcgggcac gccgcggcgc cgggggcctc 300
cgcaggcgca tggagccggt ctgcaaggaa agtgaggcgc cgcgcgtcgc ttctggagga 360
ggggggcaca aggtctggag accccgggtg gcggacggga gccctccccc cgccccgcct 420
ccggggcacc agctccggt ccattgttcc cgcccggtc ggaggcgccg agcaccgagc 480
gccgcgggga gtcgagcgcc ggccgcggag ctcttgcgac ccgcccagga ccggaacaga 540
gcccgggggc ggcgggcccg agccggggac gcgggcacac gcccgctcgc acaagccacg 600
gcggactctc ccgaggcgga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660
gagctcactg tggagtatcc atggagatgt ggagccttgt caccaacctc taactgcaga 720
actgggatgt ggagctggaa gtgcctcctc ttctgggctg tgctggtcac agccacactc 780
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gaagtggagt ccttctggt ccaccgggt g acctgctgc agttgcgctg tcggtgctgg 900
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gtgtacagtg acccgagcgc gcacatccag tggtctaaagc acatcgaggt gaatgggagc 1620
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atgaagagtg gtaccaagaa gagtgaactc cacag ccaga tggctgtgca caagctggcc 1980
aagagcatcc ctctgcgcag acaggtaaca gtgtctgctg actccagtgc atccatgaac 2040
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gacgcaacag agaaagactt gtcagacctg atctcagaaa tggagatgat gaagatgatc 2340
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gtcatcgtgg agtatgcctc caagggcaac ctgcgggagt acctgcaggc ccggaggccc 2460
ccagggtctg aatactgcta caaccacgac cacaaccagc aggagcagct ctctccaag 2520

120/292

```

gacctggtgt cctgcgccta ccaggtggcc cgaggcatgg agtatctggc ctccaagaag 2580
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ggtgacagag gacaatgtga tgaagatagc agactttggc ctgcacagg acattcacca 2700
catcgactac tataaaaaga caaccaacgg ccgactgcct gtgaagtgga tggcaccga 2760
ggcattatct gaccggatct acaccacca gagtgatgtg tggctcttcg ggggtgctcct 28 20
gtgggagatc ttactctgg gcggctcccc ataccctgggt gtgcctgtgg aggaactttt 2880
caagctgctg aaggagggtc accgcatgga caagcccagt aactgcacca acgagctgta 2940
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tgctatatat taaaacaaa aaagaaaaa aaggaaaatg tttttaaaaa ggtcatatat 4020
ttttgtctac tttgtctgtt ttattttttt aaattatgtt ctaaac 4066

```

<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

```

cagttatata cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagggtgaac cagctcctcg aggagatata 120
ccccaaaccac caggtcctac tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgatc aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccaccat gttagacagaa gatctgcccc tccaccaagg cagtgaagag aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaaacttgt gtgnatctgt cnggtcttct ggtttccctg gagga 415

```

<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

```
agagagccga gctctggagc ctcagcgagc ggaggaggag gcgcagggcc gacggccgag 60
tactgcggtg agagccagcg ggccagcgcc agcctcaaca gccgccagaa gtacacgagg 120
aaccggcgcc ggcgtgtgcg tgtaggcccg tgtgcggcg gcggcgcgagg aggagcgcg 180
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accagtggat cgagcagctg aacgagtga agcagctgtc cgagtccag gtcaagagcc 300
tctgcgagaa ggctaaagaa atcctgacaa aagaatccaa cgtgcaagag gttcgatgtc 360
cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgtttagaa 420
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attattcagt tgaaacagtt acactgcttg tagctcttaa ggttcgttac cgtgaacgca 540
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atgaatgttt aagaaaatat ggaaatgcaa atgtttggaa atattttaca gatctttttg 660
actatcttcc tctcactgcc ttggtggatg ggcagatctt ctgtctacat ggtgggtctct 720
cgccatctat agatacactg gatcatatca gagcacttga tcgcctacaa gaagttcccc 780
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tatctcctcg aggagctggt tacacctttg ggcaagatat ttctgagaca tttaatcatg 900
ccaatggcct caggttgggt tctagagctc accagctagt gatggaggga tataactggt 960
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aacttgtgaa ctaagaactg agaagggtcaa attttaattg tatcaatggg caagactggt 1860
gctgtttatt aaaaaagtta aatcaattga gtaaatttta gaattttag actttaggt 1920
aaaataaaaa tcaagggcac tacataacct ctctggtaac tccttgacat tctt cagatt 1980
aacttcagga tttatttgta tttcacatat tacaatttgt cacattgttg gtgtgcactt 2040
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agacttaatt gtaaaacat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatggt ttcaggtaga g                                     2181
```

<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185
cgaagaggat gaggaagagc tntctgtgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg gcggtnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagccccgaa gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
gggggttaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gttcctgagg 360
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186
gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
gaggaggggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcagggtg 180
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ccctgatggg tgacttogca ggcgtagact ttgtgtttct cgtagtctgc tttgtcagc 300
gtcagggtgc tgctgaggct ntagggtgct gtccctgctg tctgctctg tgacactctc 360
ctgggggant taccnattt gggagggcgt tatccacctt ccactgtact ttggc ctctc 420
tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acatttctt tgatccncca 540
ct 542

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MCLR) gene.

<400> 187
atcacctgca gctccatgct gtccagctc tgcttctg ggcacatgc gtggaccgct 60
acatctccat cttctacgca ctgnetacca cagcatcgtg accctgccgc gggcgcaag 120
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180
gaccacgtgg ccgtctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
gccgtgctgt acgtccacat gctggcccgg gcctgccagc acgccaggg cattcg 296

<210> 188

123/292

<211> 1270

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1270)

<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MCLR) gene.

<400> 188

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ggagagggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catggggggac 60
accaaggcc cctgggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggctccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
ggatcccaga gaagacttct gggctccctc aactccaccc ccacagccat ccccagctg 240
gggctggctg ccaaccagac aggagcccgg tgctggagg tgtccatctc tgacgggctc 300
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aagaaccgga acctgcactc acccatgtac tgcttcatct gctgcctggc cttgtcggac 420
ctgctggtga gcgggagcaa cgtgctggag acggccgtca tcctcctgct ggaggccggt 480
gcactggtgg cccgggctgc ggtgctgcag cagctggaca atgtcattga cgtgatcacc 540
tgcagctcca tgctgtccag cctct gcttc ctgggcgcca tcgccgtgga ccgctacatc 600
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aagtgtgctg ggcagaggga ggtggtgata ttgtgtggtc tggttcctgt gtgaccctgg 1200
gcagttcctt acctccctgg tcccgtttg tcaaagagga tggactaaat gatctctgaa 1260
agtgttgaag                                     1270
```

<210> 189

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189

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ccaanaccaa atccgagccc ttggacaaa ctgcctgcg ccgagagccg tccgcgtaga 60
gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggaag 120
aagaaggagc gaggtcgcnc aagaagccgg ntcccggggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt                                     336
```

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
tctcaacaat atgctcactg gaga tgacgt ttttagatac gtattgattc accagctgga 60
cattctcggg gggtnngtta ggatggtag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcact ctcttctggt acagctcctn cgctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
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cgggctcggc cggaggccag gagctgag cg gcggcggtg ccggacgatg ggagcgtgag 120
caggacggtg ataacctctc ccgacgcggg ttgcgagggc gccgggcaga ggccaggacg 180
cgagccgcca gcggcgggac ccacgcgaga ctcccgggg cgacaggagc agccccgaga 240
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tgagggaac gggagacgcc cccgcgcagc gcgagcgctt cagcgcggcc gctcgtcttc 360
cccacgcagg gacaaacttt tcccaaaccg gatccgagcc cttggacca actcgcctgc 420
gccgagagcc gtccgcgtag agcgtctcgt ctccggcgag atgtccgagc gcaaagaagg 480
cagaggcaaa gggaagggca agaagaagga gcgaggctcc ggcaagaa gc cggagtccgc 540
ggcgggcagc cagagcccag ccttgccctc ccaattgaaa gagatgaaa gccaggaaac 600
ggcttcgagt tccaaactag tcttcggtg tgaaaccagt tctgaatact cctctctcag 660
attcaagtgg ttcaagaatg ggaatgaatt gaatcgaaaa aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggtgattc 780
tgagagtat atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840
caccatcgtg gaatcaaacg agatcatcac tggatgcca gcctcaactg aaggagcata 900
tgtgtcttca gagtctccca ttagaatatc agtatccaca gaaggagcaa atacttcttc 960
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aactttctgt gtgaattggag gggagtgtt catggtgaaa gaccttcaa accctcagag 1080
atacttgtgc aagtgcccaa atgagtttac tggatgacgc tgccaaaact acgtaatggc 1140
cagcttctac aaggcggagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200
catcgccctc ctgtgtgtc gcacatgtg tgtggtggcc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gagccttcg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

```
tcaatacgta tctaaaaa cg tcatctccag tgagcatatt gttgagagag aagcagagac 1440
atccttttcc accagtcact atacttccac agcccatcac tccactactg tcacccagac 1500
tcctagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
aatcgtagtg tcatccgtag aaaacagtag gcacagcagc ccaactgggg gcccaag agg 1620
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caagcccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctcccagag 2160
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```

<210> 192

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. ciliary neurotrophic
factor receptor (CNTFR) gene.

<400> 192

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cagatgctac gccgggaagg agtacattat ccagggtggca gccaggaca atnagattgg 60
gacatggagt gactggagcg taccgccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tcgagagacc acgaccagca ccaccagctc cctggcacc 180
ccacctacca cgaagatctg tgacctggg gagctgggca gcggcgggg accctcggca 240
cccttcttgg tcagcgtccc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagcccg gcaccccatg aggacatgca gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtagaccccg gtttctattt t ncacacggg caggaggant 420
tttgcattn ttttnagac acaattttt gga 453
```

<210> 193

<211> 1566

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1566)

<223> ciliary neurotrophic factor receptor (CNTFR)
gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcgccgc gaggctcggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgcctcgtc gccgggggag gtcggaaggc 120
gcggcgccgaa gcccggggtgg cccgagggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtctct aagagtttgt ctggaggagg aggaggacat tgatgtgctt 240
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tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
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agcctgcaga ccccggtttc tatttt gcac acgggcagga ggacctttt cattctcttc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac aactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggctcccc atcatcgtac tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtgtt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccacccg acctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgccaaa ccacagggcc ngggatgaca gatactgtg 349

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<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(729)
<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195
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gggcctgggc gttttgttgt tggctctcgt gctg ggtctg ggtctgacct caccgacct 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggcggggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aaacctcaca gagaaaacct aagaataagc aagtcttctt tccagggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgtgttgt cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccctct gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttcccc tctgcaccca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg tttctgtttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt 729

<210> 196
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196
ngttactcca gccttggacc ggggctgcca ctt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggtcctgc cgggccactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgcacctg gggatctcga tgcctcctc atcctgcagg gtcccccta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgctggg ccagcattgt ctttatttca ttgccttcca gcttgcggtt gttaggggtg 420
cagaccttaa ccognaccgt ttccagacca tt 452

<210> 197
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcag 60
aagacagtcc tatggcttcc tggctcttgg acccggtctt gggacgcagg gctaccgtgc 120
agctgagggt gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc ttttnttgcc 360
ccggcttcga tgggtgtttt 379

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

cctggggcgg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgctgct gtcactgcc a tccattggag ccacagcacc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccgcgtccct gtgtccactt 180
ctcctgacct ctcgcccgcc accccagaag gctggagcag ggacgcgcgtc gctccggccg 240
cctgctcccc tcgggtcccc gtgcgagccc acgcccggccc cggtgcccgcc ccgcagccct 300
gccactggac acaggataag gccacgcgca caggccccca cgtggacagc atggaccgcy 360
gcacgctccc tctggtgtgt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtggggcc cgagagggg c gaggtgacat 480
ataccactag ccagggtctg aagggtctgc tggctcaggc ccccaatgcc atccttgaag 540
tccatgtcct ctctctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggccccgag aggtgcttct ggtcctcagt gtaaacagca 660
gtgtcttctt gcatctccag gccctgg gaa tccactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttccccaaga 780
cccagatcct tgagtgggca gctgagaggg gccccatcac ctctgtgct gagctgaatg 840
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tgccggggcca ctcgcccggg ccccggaagg tgacggtgaa ggtggaactg agctgcgcac 1080
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129/292

```

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```

<210> 199

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(402)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 199

```

tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgttgtc tataatgaaa 60
acaaatcagg caattttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402

```

<210> 200

<211> 4877

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4877)

<223> epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 200

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gtcacagtga agtcagcca agcagggtcg ttaaactctg tgaaatttgt cataagggtg 180
tcagggtattt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtgcttc 240

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ggagccccag ttatgtggaa tgggcacaga

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taagggctcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gaccttgaa ggggtgtcg agaagccca ttctctcta tcagctaacc cattatggca 4020
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aaaatcacca aaaacat 4877

<210> 201

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(153)

<223> 3' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 201

attagacctc acattagga aaacatcaaa atgancacg cagaccctt gagatcctga 60
ggttggccca gccgagccg tgctcagaag ccccccagct cgggccccca gctgcccga 120
cgcccgcct caccagcagg caggtcccca tcc 153

<210> 202

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 202

agtgaatgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgtg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttata ctgagacaaa ccactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaac atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

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aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatcctc agtctcttnt tgttgacat tttgcgtggc nt 472

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

cactgcgctt gcgcgggttg agggcggttg ctacgtctcc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcagggagaa gagcctgctg agtgacgtga ggcgggtctc 240
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gattgtgtgt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
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atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttgggtgcc atcgacatg ctcaataaat attttaaatg agtgaaaaaa aaa 2093

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

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tgggggcctt tattaaggct tggcagatgt ggtggagggtg gaagtacaaa ccagggcctg 60
ggcctaggaa agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccctt catcccaggt tcctttcttc aacctccgcc tgctcttggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccagggn ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctctg ccagtatgaa gttggggaag cgcttttctc tgtccccagc aacagaacaa 360
actcttgttc tctgtgggtt ngggggaaaa ggttngggg ggtttggact taggggagaa 420
gttnagcttg a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

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aatttcctga gatcctcttg cacctcccag cccacccttg gccatgggta cctcggggaa 120
catagctccg tcttcagca gccctggga catttgccac tccttcacat cttagggagg 180
gggcggggaa cccctcccag gcccctacc aacaccagct gtccgagccc tgcccacct 240
atcccagca gagctttaag caagaatacc atgatccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggtgggggt tcaatggggg cacagggtac ccaggggggn 360
ggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnttaag gatttnaggt 420
tntttaancg ggttg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

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agacccagct cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
cagggcactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacia 240
acgtggacat gtactcgcc cagagagatg cccaggagc tgtatgcgn cgggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcnccacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcnggac 420
attntagaa gagcatctgc ccggaga 447

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

gctgctgcgc ccgcggtctc ccagtgcgcc gagtgccccg cgggccccgc gagcgggagt 60
gggacccagc cctaggcaga acccaggcgc cgcgccccgg acgccccgcg agagagccac 120
tcccgccac gtccatttc gcccctcgcg tcoggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcgccagg tggctaccca ccagctgcac caggtggtgg 240
tccctgggga ggtgctgcct accctcctcc gccagcatg ccccccacg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
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tcaccgtcct agagcttagg cctgtcttcc accctcctg acccgatatg tgtgccacag 1860
gacctgggct ggtctagaac tctctcagga tgcctttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatggt tcatttttct gaaaaaa 1958

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

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gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tctcctgggg caaaagggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgagggt ttic gticga agacagaatt 360
ggacagttga ggacagttat tgtcttntt taaaagnaca aggaagggtt cagnttgggt 420
tacccecaag gag                                     433
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<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

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 gtaaatgtgc cagtgtggag tggccacgtg tgtgtgccag tatatggccc tggctctgca 4560
 ttgacactgc tatgaggctc tggaggaatc cctcaccctc tctgggctc agtttccct 4620
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 catcctgggg gtcagctggg ctccctgggag attccagatc acacatcaca ctctggggac 4800
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 cttgacttag agtgacagcc ggtgtcctgg aaagcccaa gcagctgcc cagggacatg 4920
 ggaagaccac gggacctctt tcaactacca cgatgacctc cgggggtatc ctgggcaaaa 4980

137/292

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gggacaaaga gggcaaatga gatcacctcc tgcagcccac cactccagca cctgtgccga 5040
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cttcagatgg taccccaaga aggatgtgag aggtggccgc ttggagtttg cccctcacc 5160
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ttacaaatat ttttaggact cacgttaact cacatttata ca gcagaaat gctattttgt 5520
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<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSCR14) gene.

<400> 210

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gaccggcgta tcacacacat ctccgcgga caggagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcatgggct cgtgagcaca ctcaagtccc agcccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgcaag aggaggccca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccgccac aggggtaccc attcacacac cagcgttttg 300
accagatgag agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
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<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSCR14) gene.

<400> 211

```

ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgcccagccc agactcggac 120
tcggacacag actcggagga cccgagtcct cggcgagcag g cggggcggtt gctccgctcg 180
caggatcatc acagcggta cttcatggtg tcgtcgccgc acagcgactc gctgccccgg 240
cggcgcgacc aggaggggtc cgtggggccc tccgacttcg ggccgcgag tatcgacccc 300
acactcacac gcctcttcga gtgcttgagc ctggcctaca gtggcaagct ggtgtctccc 360
aagtggaaag atttcaaagg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggta tatccagtat gtgaagcggg ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
ctggagggga actactggaa gcggcgcatc gaggtggtga tgcgggaata ccacaagtg g 600

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138/292

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cgcatctact acaagaagcg gtcocgtaag cccagcaggg aagatgacct cctggcccct 660
aagcaggcgg aaggcaggtg gccgcgcgg gagcaatggt gcaaacagct cttctccagt 720
gtgggtcccg tgctgtggg ggacccagag gaggagccgg gtggggcgga gtccttgac 780
ctcaattgct ttttgccga catctcagac actctct tca ccatgactca gtccggccct 840
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gacctgacgc cactgcagcc aagcctggat gacttcatgg acatctcaga tttctttacc 960
aactcccgc tcccacagcc gcccatgcct tcaaacttcc cagagccccc cagcttcagc 1020
cccggtggtg actcctctt cagcagtggt accctggggc cagaggtgcc cccggcttcc 1080
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agcagggcag gcatcatg tg tgtgtgtgtg tgtggatgtg tgtgtgtggg ttttgtaaag 3240
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<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 212

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cctttggcct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cctttctgcc 120
gacccctagt tccctctgct cagccaagct tggtatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207
```

<210> 213

<211> 1304

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1304)

<223> cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 213

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tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctggggc gccgccctgg 120
ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcctggtgac 180
ctgctctctc gctggccagg ccaccaccgc ct acttctctg taccagcagc agggccggct 240
ggacaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgag catggccacc ccgctgctga tgcaggcgct 360
gcccatggga gccctgcccc agggggccat gcagaatgcc accaagtatg gcaacatgac 420
agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtgt acccgccact 480
gaaggggagc ttcccggaga acctgagaca ccttaagaac accatggaga ccatagactg 540
gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcactcctt 600
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tggtctgggt gtgaccaagc aggatctggg ccagtcctcc atgtgagagc agcagaggcg 720
gtcttcaaca tcctgccagc ccacacagc tacagctttc ttgctccctt cagccccag 780
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ggacccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304
```

<210> 214

<211> 355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(355)

<223> 5' terminal sequence. annexin a7 (ANXA7) gene.

<400> 214
aggaaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctccataggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatcctn ggccctcttc 240
atgcctccta cgtattacga tgccctngagc ttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatatt ngtgcacang atcanattca ggtaa 355

<210> 215
<211> 2176
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2176)
<223> annexin a7 (ANXA7) gene.

<400> 215
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atgtcatacc caggctatcc cccaacaggc taccacactt tccctggata tccctctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatcctt atcctagtgg ctttctcca 180
atgggaggag gtgcctaccc acaagtgcc aagtagtggt acccaggagc tggaggctac 240
cctgcgcctg gaggttatcc agccctgga ggctatcctg gtgcccaca gccagggga 300
gtccatcct atcccgaggt tccctcaggc caaggatttg gaggccacc agg tggagca 360
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ccactacctg gtggctttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttacccta gtcagatcaa tacagattct ttttcttcc atcctgttt ctctcctgtt 540
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caaaaaatta aagcagcatt taagacctcc tatggcaagg atttaataca agatctcaa 780
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aataattttt taga aggtta ctgaaagctc tgcttccgg aatccctcta agtctgcttg 1920
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ataaaaaatt gcatat 2176

<210> 216
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(525)
<223> 3' terminal sequence. thrombospondin 1
(THBS1) gene.

<400> 216
tcctgnanta nctncaacaa ccgatgtgag ggaaaatcgg tccagacacg gacctgccac 60
ttatcaggagt gtgacaagag atttaaacag gatggtggct ggagcntgng ttccccgtgg 120
tcatcttggt ctgtgacatg tggatggtgt gtgatcaciaa ggatccggct ctgcaactct 180
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ctctgccag ctggttcctt gggcatct gc agcctgcagt ttcagtggg tcataggagc 360
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gaggcagagg ttttttgaac ggnnttaggg gatttttgc aagtt 525

<210> 217
<211> 5722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5722)
<223> thrombospondin 1 (THBS1) gene.

<400> 217
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cgccgcgctc cgttacacac aggatccctg ctgggcacca acagctccac catggggctg 120
gcctggggac taggcgtcct gttcctgatg catgtgtgtg gcaccaaccg cattccagag 180
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gccaacctga tccccctgt gcctgatgac aagttccaag acctggtgga tgctgtgcg 360
gcagaaaagg gtttctcct tctggcatcc ctgaggcaga tgaagaagac ccggggcacg 420
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gaagaagctc tcctggcaac cgccagtggt aagagcatca ccctgtttgt gcaggaagac 600
agggcccgag tgtacatcga ctgtgaaaag atggagaatg ctgagttgga cgtccccatc 660
caaaagcgtc tcaccagaga cctggccagc atcccgagac tccgca tcgc aaaggggggc 720
gtcaatgaca atttccaggg ggtgctgcag aatgtgaggt ttgtctttgg aaccacacca 780
gaagacatcc tcaggaacaa aggtgtctcc agctctacca gtgtcctcct cacccttgac 840
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 aatgataaaa ttccagatga cagggacaac tgtccattcc attacaacct agctcagtat 2400
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 gaagatggcc accagaacaa tctggacaac tgtccctatg tgccaatgc caaccaggct 2760
 gaccatgaca aagatggcaa gggagatgcc tgtgaccag atgatgaca cgatggcatt 2820
 cctgatgaca aggacaactg cagactcgtg cccaatcccg accagaagga ctct gacggc 2880
 gatggtcgag gtgatgcctg caaagatgat tttgacctg acagtgtgcc agacatcgat 2940
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 cctctggacc ccaaagggac atcccaaat gaccctaact gggttgtacg ccatcagggt 3060
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 aatgctgtgg acttcagtgg caccttcttc atcaacaccg aaaggacga tgactatgct 3180
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taggcttcat acggaagt g tttgagagca agtagttgac atttatcagc aaatctcttg 4860
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atgttatggg attccttttt tctctgtttt atcttttcaa gtggaattag ttggttatcc 4980
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tcccttggtg atatttccag ggagaaggaa agcatataca cttttttctt tcatttttcc 5100
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ctatttgcca ataccttttt ctaggaatgt gctttttttt gtacacattt ttatccattt 5640
tacattctaa agcagtgtaa gttgtatatt actgtttctt atgtac aagg aacaacaata 5700
aatcatatgg aaatttatat tt                                     5722

```

<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

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ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catctcatac actcattaac aacacttaac 120
acatccaatt aaagggtctg caaagtcttc tgctgggtgg tgctcttcat cccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagaggggta ggcgagcctc 240
actttagttt ccggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggctgc aggaatattc tcaagggtcat ggaatattag ggngtctggg ncaat cttgg 360
ggcccttttt tcttttttcg ttncatttct ccattta                                     397

```

<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

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ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggg agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180
gatcaactga gattctcata catggctata atagaaggag caaaatgtat aaaggagat 240

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tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220

<211> 2287

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2287)

<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220

ggggggcctg agcctctccg ccggcgcagg ctctgctcgc gccagctcgc tcccgcagcc 60
atgccacacca ccctcgagcg ggagttcgaa gagttggata ctacagctcg ctggcagccg 120
ctgtacttgg aaattcgaaa tgagtcocat gactatcctc atagagtggc caagtttcca 180
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240
ctgcaaaatg ctgagaatga ttatattaat gccagtttag ttgacataga agaggcacia 300
aggagttaca tcttaacaca ggttocactt cctaacacat gctgccattt ctggcttatg 360
gtttggcagc agaagaccaa agcagttgtc atgctgaacc gcattgtgga gaaagaatcg 420
gttaaatgtg cacagtactg gccaacag at gaccaagaga tgctgtttaa agaaacagga 480
ttcagtggtg agctcttgtc agaagatgtg aagtcgtatt atacagtaca tctactacaa 540
ttagaaaata tcaatagtgg tgaaccaga acaatatctc actttcatta tactacctgg 600
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gatattaaca taaaacaagt gttactgaac atgagaaaat accgaatggg tcttattcag 840
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tgaaaaatct gttactaaaa aaaaaaattg tatgtcgatt gaattgtact ggatacattt 1920
tccatttttc taaaaagaag tttgatatga gcagttagaa gttggaataa g caatttcta 1980
ctatatattg catttctttt atgttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
aaagaacaaa aagtttttcc taaaaaatc tttgaaggaa aattctcctt actgggatag 2100
tcaggtaaac agttggtcaa gactttgtaa agaaattggt ttctgtaaat cccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280
taaaccc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgta tcttcattga gctcaagttt 180
actgtacgtg actgcaacag cttccctggg tggcgccant tcctggcaag gagactttca 240
accttacta tgccgagtcg gacctgggac tacggcanca acttncagaa gcgcct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
cggaagttgc gcgcaggccg gcgggcgggg ggggacaccg aggccggcgt gcaggcgtgc 60
gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcatggagc 120
tccaggcagc ccgcgcctgc ttgcacctgc tgtggggctg tgcgctggcc gcggccgcgg 180
cggcgagggg caaggaagtg gtactgctgg actttgctgc agctggaggg gagctcggct 240
ggctcacaca ccggtatggc aaaggggtgg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggctccgca 360
ccaactgggt gtaccgagga gaggtgagc gtaacaactt tgagotcaac ttactgtac 420
gtgactgcaa cagcttccct ggtggcgcca gctcctgcaa ggagactttc aacctctact 480
atgccgagtc ggaacctggac tacgg cacca acttcagaa gcgcctgttc accaagattg 540
acaccattgc gcccgatgag atcacgtca gcagcgactt cgaggcacgc cactggaagc 600
tgaacgtgga ggagcgctcc gtggggccgc tcaccgcaa aggtttctac ctggccttcc 660
aggatatcgg tgccgtgtgt gcgctgctct ccgtccgtgt ctactacaag aagtgcctcc 720
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agagccgagt gtggaagtac gaggtcactt accgcaagaa gggagactcc aacagctaca 1560
atgtgcgccg caccgagggt ttctccgtga ccct ggacga cctggcccca gacaccacct 1620

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gagcccatc ggccaagaat acttgaagaa acagagtggc ctccctgctg tgccatgctg 3120
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agttgcagat gattcaaac g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

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ggaacagggt ggacactgtg caggcttcag cttccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctcccg aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

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cagtntaggt cttggtnaag ccccgcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360
tcctcggtng cggtttttgg ggaccnttgg aagtntc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc 437

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

gccncagatc cagcgccag agagacacca gagaaccac catggcccc tttgnagccc 60
ctggcttctg gcatectgtt g ttgctgtgg ctgatatgcc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagtgc 180
gtggggacac cagaagtcaa ccagaccacc ttataaccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
ccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagtgt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagtttng 420
tgggttcctt gggaacagtc tgaggtttag tttagcggtn ggggtt 466

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

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ccatggcccc ctttgagccc ctggcttctg gcatectgtt gttgctgtgg ctgatatgcc 120
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataaccagc 240
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300
acatccggtt cgtctacacc ccgccatgg agagtgtctg cggatacttc cacagggtccc 360
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gcaaaactgca gattggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600
agggcttcca gtcccgtcac cttgcctgcc tgcctcggga gccagggtctg tgcacctggc 6 60
agtccctgcg gtcccagata gcctgaatcc tgcccggagt ggaactgaag cctgcacagt 720
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gc

782

<210> 226
<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(353)
<223> 5' terminal sequence. ephrin -a1 (EFNA1)
gene.

<400> 226
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120
agaagagact tgcagcagat gaccagagg tgccgggttct acatagcctc ggtcacagtg 180
ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttccactt ctgctgctgc 240
aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
caggcactcc aaacctgtct tgggggccac ttccagagcc ccagccctt ggg 353

<210> 227
<211> 1480
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1480)
<223> ephrin-a1 (EFNA1) gene.

<400> 227
gcggagaaag ccagtgggaa ccagagccca taggagaccg gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacacccg tcttctggaa cagttcaaata ccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtcgcg tggcagtgc accggcccag 360
tgccaagcat ggcccgagga agctgtctga gaagttccag cgcttcacac ctttcacct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
acatagcctc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
ccttccactt ctgctgctgc aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagcc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaacagg 840
gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tccttaagg cacagtggga gctgagctgg 1020
aagggggcac gtggatgggc aaagcttgct aaagatgccc cctccag gag agagccagga 1080
tgccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgacca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggtact gcattctctc ccattcctgg gcagcactcc 1260

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```
ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaat aaagcaatgt gttttttcgg 1480
```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```
ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatctct gctagtaaac cacagttact taccagtcca taaataaaat 170
```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```
gaattcgcgg ccgcctcttg cgggtcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcata ccgctggtct gacgattgtg gagaggcggg ggagaggcctt 180
catccatccc acccggtcgt cgccggggat tgggggtccca gcgacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcccgcgc 300
cggagcccgg gacaccggcc accctccgcg ccacccaccc tcgctttctc cggcttctct 360
tggcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaa cagcacaagt gcaataagag atatttcctc aaatttgctt 480
caagatggaa accctttgcc tcagggcatc cttttggct g gcaactggtg gatgtgtaat 540
cagtataaat cctgagagat acagcacaaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttcttggt taccactcat caaccacta atttggtcct 660
accagcaat ggtcaatgc acaactattg ccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcata gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgctgat 840
agccagtctt gcccttggag acqttatcta tgttggtcatt gatctcccta tcaatgtatt 900
taagctgctg gctgggcgct ggccttttga tcacaatgac tttggcgat ttctttgca a 960
gctgttcccc tttttgcaga agtctctcgt ggggataccc gtcctcaacc tctgcgctct 1020
tagtgttgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttggttaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tgggtaccct tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtctaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260
```



```

cttcgggttc tattttctgta tgcccttggt gtgcactgcg atcttctaca ccctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttggtt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatatgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggaac 1560
catgaattca tgtataaacc ccatagctct gtattttgtg agcaagaa at ttaaaaattg 1620
tttcacgtca tgcctctgct gctgctgtta ccagtcctaaa agtctgatga cctcgggtcc 1680
catgaacgga acaagcatcc agtgggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcaactcctc gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cggaatctc ttctctgatc 1860
cttcttctct aattcactcc cacacccaag aagaaatgct ttccaaaacc gcaaggtaga 1920
ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgcgtgt tgtattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
aaatgaaccc agaaggatat ttactacttt tgcattgaaa tagagcttc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatggt caatgggaac tggtcacat gaaactttag 2160
agattaacga caagattttc tacttttttt aagtgatttt ttgtccttca gccaaacaca 2220
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taatagccta acatgattat ttgaacttat ttacacatag ttgaaaaaaa aaaagacaaa 2340
aatagtattc aggtgagcaa ttagattagt attttccacg tcaactattta tttttttaa 2400
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atgggttttt attacaaggg acctgaaca tgttttgtat gttaaattca aaagtaatgc 2580
ttcaatcaga tagttctttt tcacaagttc aatactgttt ttcatgtaaa ttttgtatga 2640
aaaatcaatg tcaagtacca aaatgttaat gtatgtgtca ttttaactctg cctgagactt 2700
tcagtgcact gtatatagaa gtctaaaaca cacctaagag aaaaagatcg aatttttcag 2760
atgattcgga aatttttcatt cagggtattt taatagtgc atatatatgt atatacatat 2820
cacctcctat tctcttaatt ttgtttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagttta tcatgtcagt 2940
gaaaaataat taccacaaaa tgccaccagt aacttaacga ttcttcaact cttgggggtt 3000
tcagtatgaa ctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
ggcccacagt gacttttgcg ggcatttttc ccagatgttt acagactgtg agtacagcag 312 0
aaaatctttt actagtgtgt gtgtgtatat atataaaca ttgtaaattt cttttagccc 3180
atttttctag actgtctctg tggaatatat ttgtgtgtgt gatatatgca tgtgtgtgat 3240
ggtagtatg gatttaattc aatctaataa ttgtgcccgc cagttgtgcc aaagtgcata 3300
gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
agaggcagcg tgaaagcaga tgagctgtgg actagcaata tagggttttg tttggttgg 3480
tggtttgata aagcagttat tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag tattatattg ttcttatcct caattcaatg tggatgatgaa attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgctg ataataaatt aggtgaagata 3660
atgtgttggg ccatatttta ggacaggtaa aataacatca gggtccagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca tttgttttag 3840
acaattgtct ttttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg ccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

```

<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggttttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc ccctcccacc ccctaaagt ccaaccaaag tgagaggggc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatcccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggcccttc ttatccgaga gagtgaagag gctcctgggg acttctccct ctctgtcaag 180
tttggaacag atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tggttggtga agttcaattc ttgga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgtcca ggggcctttt ttgattttt gattccccag gggggnttgg ngaggttggg 420
ttttccgcgc ggggagattt tattccatgt tcntgggtn aatttaggaa ccntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2
(GRB2) gene.

<400> 232

gccagtgaat tcgggggctc agccctctc cctcccttcc cctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaaag gggggacatc ctcaaggttt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40
atgaaaccac atccgtggtt ttttgcaaaa atccccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttctctg ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatatcc tgccggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttagctttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattgata actcagaccc caactggtgg 660

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```
aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgtagac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tgcccggtgc accctgtgac cctctcactt tgggttgaac tttagggggt gggagggggc 900
gttggaattt aaaatgcaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tactgtctgc tctcttttcc cctcctttgt ctttttttcc atcctttttt ctcttctgtc 1020
catcagtgc tgaagttaa ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaa aaaaaaaac ccgaattca 1109
```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```
cgcgctctc ggctgcnng ntgtacaccg cgccgaaag tggggctccg agggggcgca 60
ctcaaaaccc tgccttttct ttacttttac ttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgccctttc ctgatctcg ctccccctt cggttcttc gaccgggtcc cccctccctt 300
ttttgttct gttttgtttt gttttgctac gagtccacat tctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttccca 446
```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```
ccgaggctat aagagggcgc acaagtggcg cggcgaggga gccgccgcca gtggagggcc 60
gggcgctcgc gccgcggccg gggcgggcgc agggccgagc ggacgggggg gcgcggggcc 120
cccgaggagc cgcggccact ccccccggg ccggcgcggc gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggctggggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc ccggggcggc ccccgacggc cgcggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc cgcgcgccgc ctctacccc cctgccgcgc acggcgcccc cagcgcggca 420
ccccccgagc gctcgtcgc ctctcccgac ctggggctgc tgaagctggc ctcccccgag 480
ctcagcgccc tcatcatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gagcaggagt tcgccgaggg cttcgtcaag 600
gccctggagg atttacacaa gcagaaccag ctcggcgcgc gccgggc cgc tgccgcgcgc 660
gccgcgcgc ccggggggcc ctcgggcacg gccacgggct ccgcgcccc ccgcgagctg 720
```

153/292

```

gccccggcgg cggccgcgcc cgaagcgcc gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgccgccgc cccccccagg cgcgt tgggg ccgcgcgcc tggctgcgct caaggacgag 900
ccacagacgg tgcccgcagt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
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tccaagtgcc gcaagcgcaa gctggagcgc atctcgccgc tggaagagaa agtgaagacc 1080
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cagctcaagc agaaagtcct cagccacgct aacagcggct gccagctgct gcccagcac 1200
caggctccgg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcggggg 1260
ggtgtctgtg gcgccccgga cttggagagg gtgcggccct ccaccccccc ctcccagat 1320
gtgcccagga actcagagag gcgcggcccc ggggattccc ccccgaggtg cccaggactc 1380
ggaagggcg ccccgactc gacaagctgg acccctgct cccggggcg agcgcatgac 1440
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gcgtctcggc tgccc ctttg tacaccgcgc cgcaagggg ctccgaggg gcgcacgtca 1560
aaccctgcct ttcctttact tttactttt tttttcttt ggaagagaga agaacagagt 1620
gttcgattct gccctattta tgtttctact cggggaacaa acgttggtg tgtgtgtgtg 1680
tgttttcttg tgttggttt ttaaagaaat gggaagaaga aaaaaaatt ctcc gccct 1740
ttcctcgatc tcgctcccc ttcggtctt cgaccgtccc cccctccct tttttgttc 1800
tgttttgttt tgttttgcta cgagtccaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgttt cagtaaagtc tcgttacgcc a 1891

```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```

accaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaccc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tcctggntca 240
ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggaggggggc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg ccntcgaaga cggcatttng gaggaattng aagaggaata c ggtaagaa 420
g 421

```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```

tgccaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccaggttg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggtcgcc taggtccgg tacttatgat tacgaatcct ttcctttatt ttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc tttccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cactatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggaggggc 420
gcctcttctc ttcttagg                                     438

```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

```

aaaaattttc tgttacaaa ttttacaact tctaataaga ctactataac tttatgtaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatgtt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaatgt aaaatatttg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgcctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccagggc cttcgccggg gcctgggcct 360
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agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga agcatgcat caaatgcata agcccatcga tggatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcacccag gcatggccc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccca gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cactcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtctgtcca gctgcatcag 840
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ctgcagcttg cagtccaggg gaaaaggacg ttgcctggct tgcagcaaca acagcagcag 960
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agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ccttttgcag cagaccgatg agtatgtagc caatctgacc 1920

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
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gcactgggtt gttcttatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtgt aaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaagat tcagattgaa acaaacaaaa agctttt 5257

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

```
tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac ctccggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgggaggcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcc aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tctcatcag tgggtgtgact 120
ttcttccct ccttgcatg cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttgttggg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cagccgggcc 360
cttgcccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncagntca agtnccnttt ggtnttnccc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttccct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnngganntg cctgtgacaa ttgccccaac gttccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcaggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcactgtcg gggacatcta cctcttatcc 180
accttccgcc tgcccccaa gcagggtggt gtccctcttg g cctctatcc tcgccaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaagt ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactcoga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaaact gggtgaccaa catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggccttg tggaattctat gaaaattatt ctgggtgggt ccatggcccg ggtagggagcc 600
ctgagtgagt gtccattcca aggggacgag tccatccaca gtgcagtac caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcaacc aactcaccct cttcaaccag 720
atcctggttg agctgcggga tgatatacga gaccaggtaa aggaaatgtc cctgatccga 780
aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagccc 840
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ctgttcccca acaaagacca gcagaactca gatacagatt catgttggtga tgcctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
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tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgccca 1920
cagctgcca atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctggtcccca taactgccgc 2040
```


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```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgctc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtcctcaac cagggcatgg aaatcgttca gaccatgaac 2280
agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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tgcttctccc aagaaaacat aatttgggtcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 242

```

cacttttatt ttnocttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggacttttc aacctggac aggacccgca agncaaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctggttt cnggttacag gtttcagggt cattttnttt tcggaggggt tnttcccggt 480
tcgtgagggt aggctgagggt tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial S equence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 243

```

gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatctgt gcctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc ccctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

gtctcagtcg ccgctgccag ctctgcact ctgttcttcc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgctgtggt cattgacaat ggctccggca 120
tgtgcaaaagc tggttttgct ggggacgacg ctccccgagc cgtgtttcc t tccatcgtcg 180
ggcgccccag acaccagggc gtcatgggtg gcattgggcca gaaggactcc tacgtgggcg 240
acgaggccca gagcaagcgt ggcatcctga ccctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac ctctacaac gagctgcgcg 360
tgcccccgga ggagcaccca gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaacac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgctctg ggcgcaccac tggcattgtc atggactctg 540
gagacgggggt caccacacag gtgcccactc acgagggcta cgccctcccc cagccatcc 600
tgctgtctga cctggctggc cgggacctga ccgactacct catgaagatc ctactgagc 660
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tgtgtctacgt cgccctggac ttcgagcagg agatggccac cgccgcatcc tcctcttctc 780
tgagagaagag ctacgagctg ccgatggcc aggtcatcac cattggc aat gagcggttcc 840
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cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattaggc cccagcaaca cgtcattgtg taaggaaaaa taaaagtgtg g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgccgccgg gcagctgtgc ttgctctacc tgtcggcggg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gccccgccgg agnaagcgct tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttataaacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagttgg atngggggtc aacgtccaga 360
gccaaagggtc agggggcaag gtcgtgacat gtgttnaccc tattgaaaaa aggcagcatt 420
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg tcttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcggtgag 120
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cttccttgc tcttgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcattggc 240
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gccagtgcac gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
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<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (ITGA6) gene.

<400> 247
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<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

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tgacaggtgg gccnagggg tcggggtnac cccccccag natggcagca tgatttntnt 300
acaatcaatc catcatntgg ggcacagggt ggttttcggg ggctatttnt tggctttggc 360
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<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2102)
<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

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at 2102
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<210> 250
<211> 365
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(365)
<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250
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tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
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 ctctt 365

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence, activating
 transcription factor 3 (ATF3) gene.

<400> 251

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 gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
 aagaaaacta ggcaatgtac tcttccgatg tttgtgtcac acaacactga tgtgactttt 180
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 aattctccca ggcgttaaca caaaatccat ggggcagtat ggatgggcag gtcntctgt 360
 tggcaaaactc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
 agggtttagg ggcttttcca cttcaatgtc tta 453

<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
 gene.

<400> 252

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 aagcagcatt tga tatacat gctcaacctt catcggccca cgtgtattgt ccgggctcag 780

165/292

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aatattgtg gtaaaa
2056

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<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

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502

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<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

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ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggaccac ttccccagt 1620
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<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

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ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagctttc ccatttctta gaggaaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc ttgaaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggaagggt catggcaaga naggcaggac aggcaagggg 360
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ggaaggtttg a 431
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<210> 256

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
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caatattctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggagggt tgtggacaaa 240
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tgcgttcctc atccatgcag ataacagctg gttggccggt gtggccctgc aagggcggtg 840
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cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacccatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020
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gcgttcaata aaaa 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp-binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagtttaaac tatgatttct 60
ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagt tttgctttta 180
actttgaata aatgtcatat ctaaacaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgcttctg tccagcctgg aactgacca ttgaaaaata gatgcctttc 300
tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtagcaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggct tcttgacaa ctttttcacc tactgtatcc agagctgacg 480
tggctcatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgcg 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
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aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggcggggagc agtcatctgt ggtgaggctg attggctggg caggaaacagc gccggggcgt 240
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cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtgttt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtc aaacatc actaatagaa gtgatataca 720
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aagaattgat gatcctgaaa caaacgcaca gaatagtaac ttgttttcac tattgtttct 2700

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caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggtact gtaactgact 4560
gccttgctaa aagattatag aagta gcaaa agtattgaa atgtttgcat aaagtgtcta 4620
taataaaaact aaactttcat gtc 4643

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<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

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caacctttat agtgttatgt caaataggct tgacataagc ttaaataaat atatacttta 60
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aactgggtat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
aacaatttca aagaaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
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tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttcnt cacantccct cagggtnggg ggcgggttng ggnattacc ggcgggggt 480
tttttc 486

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<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
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tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctgagtgttc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaagga tattttcttc caagcaaagg 180
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ttcgacagct gattacacag ttcctgtcat aaggaatgaa taattaatta tccagagttt 360
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<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ccaaaacgga aagtatttca agcctaaacc tttgggtgaa aagaactctt gaagtcatga 120
ttgcttcaca gtttctctca gctctcactt tgggtgcttct cattaaagag agtggagcct 180
ggtcttaca cactccacg gaa gctatga cttatgatga ggccagtgtt tattgtcagc 240
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tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
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gcattagaaa tttagctgtgt gaaataccag tgtggtttgt gtttgagttt tattgagaat 3720
tttaaattat aacttaaaat attttataat ttttaaagta tatatttatt taagcttatg 3780
tcagacctat ttgacataac actataaagg ttgacaataa atgtgcttat gttt 3834

```

<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcgtt gt ctataatg 60

172/292

```
aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaaaa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatTT taaaatanaa tgttttcatt caaatatttt aaaaaataag 240
natctaattct gaaaaaatca gtttcta 267
```

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```
ggagtccgag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tncgcgccta cgacgagcag acgcaggcct tcatcgatgc tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
caaganattt cttttgactt tggccccaac ggnagttttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc ccttcaagct tgtnttcgna 300
gaaacccaaa ctcggggggt ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt 383
```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```
ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct cgggcctcgt 60
cgtgaagaca cagcgcatct cccgcgtgta ggctttctcc acagaaccgg ttctcggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacctatgt gctgggcccgt 180
ggaggtaaac agggcccggg gcgtctccct caccaatcat cacttctacg atgag tccaa 240
gcctttcacc tgctggagc gtctggccac catccattt gatcaggta acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagcccct gtatatcccc tccaaccggg tcaacgatgg 420
tgtttgtgac tgctgcatg gaacagacga gta caacagc ggcgtcatct gtgagaacac 480
ctgcaaaagag aaggggccgta aggagagaga gtccctgcag cagatggccg aggtcaccgg 540
cgaagggttc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaaag ctcatggag tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
gctgcggaca gtgaaggagg aagctgagaa gccagagaga gaggccaaag agcagcacca 720
gaagctgtgg gaagagcagc tggctgctgc caaggcccaa caggagcagg agctggcggc 780
tgatgccttc aaggagctgg atgatgacat ggacgggacg gtctcgggtga ctgagctgca 840
gactcaccgg gagctggaca cagatgggga tggggcggtg tcagaagcgg aag ctcaggc 900
cctcctcagt ggggacacac agacagacgc cacctctttc tacgaccgcg tctgggcccgc 960
```

```

catcagggac aagtaccggt ccgaggcact gcccacogac cttccagcac cttctgcccc 1020
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gagcttgccc tccctgggcc cccaccttg gtgactcgcc ccaccacccc cagccct gtc 1980
cctgccccc ctctagtgg ggactagtga atgacttgac ctgtgaccto aatacaataa 2040
atgtgatccc ccaccc                                     2056

```

<210> 265

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. diphtheria toxin
receptor (heparin-binding epidermal growth
factor-like growth factor) (DTR) gene.

<400> 265

```

ggttctgtga ccatctgtga gtaatttatt gtctgtctac atttctgc ag atcttcctg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgccct aggcgatttt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctccccgt gtctctctcc 240
tgccaagtct cagaagaggt tgggctt cca tgctgtagc tttcctggtc cctcaccccc 300
atggccccag gccacagcg tggagactnc actttncctt tgtgtcaaga catttctctn 360
aactcctgnc attcttctg                                     379

```

<210> 266

<211> 2360

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding
epidermal growth factor-like growth factor) (DTR)
gene.


```

<400> 266
gctacgcggg ccacgctgct ggctggcctg accta ggcgc gcggggctcg gcggccgcgc 60
gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccgg 120
ccaggcttgc acgcagaggc gggcggcaga cgggtgcccgc cggaatctcc tgagctccgc 180
cgcccagctc tggtgccagc gcccagtggc cgcgccttcg aaagtgaactg gtgcctcgcc 240
gcctcctctc ggtgcgggac catgaagctg ctgccgtcgg tgggtgctgaa gctctttctg 300
gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
gctgctggaa ccagcaaccc ggacctccc actgtatcca cggaccagct gctacccta 420
ggaggcgggc gggaccggaa agtccgtgac ttgcaagagg cagatctgga cctttt gaga 480
gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
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gacttctgca tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctccctgcac 660
tgccacccgc gttaccatgg agagagggtg catg ggctga gcctcccagt ggaaaatcgc 720
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tgtctgctgg tcatcgtggg gcttctcatg tttaggtacc ataggagagg aggttatgat 840
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ctcaaggaat cggctgggga ctgctacctc tgagaagaca caaggtgatt tcagactgca 960
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gtatgctgtc atggtcctt ctggaagtt ctggtgccat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

```

aggagtgcc cggctgcccc tcacctgtg gcaagtacat ctctgcgcc gactgcctga 60

```

agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagag ggct gctgggtggc 180
ctacacgctg gacgagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggatcatc gggaaggctc tgatccacct gacgacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
lymphocyte function-associated antigen 1;
macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
gene.

<400> 268

cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgccgc ggact ccagc 60
acaccgagg acatgctggg cctgcgcccc cactgctcg cctgggtggg gctgctctcc 120
ctcgggtgcg tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
atcgagtcgg ggcgggctg cactggtgc cagaagctga acttcacagg gccgggggat 240
cctgactcca ttgctgcga caccggcca cagc tgctca tgaggggctg tgcggctgac 300
gacatcatgg accccacaag cctcgtgaa acccaggaag accacaatgg gggccagaag 360
cagctgtccc caaaaaagt gacgctttac ctgcgaccag gccaggcagc agcgttcaac 420
gtgaccttcc ggcgggccaa gggctacccc atcgacctgt actatctgat ggacctctcc 480
tactccatgc ttgatgacct caggaatgtc aagaagctag gtggcgacct gctccgggcc 540
ctcaacgaga tcaccgagtc cggccgcatt ggcttcgggt ccttcgtgga caagaccgtg 600
ctgccgttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg 780
ctggacgcca tgatgcagg cgccgctgc ccggaggaaa tcggctggcg caacgtcacg 840
cggctgctgg tgtttgccac tgatgacggc ttccatttcg cgggcgacgg aaagctgggc 900
gccatcctga ccccaacga cggccgctgt ca cctggagg acaacttga caaggaggc 960
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ggccctttg ggaagaactg cagcgcgccg tgtcc gggcc tcagctgtc gaacaacccc 2040
gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc ctacacgctg 2100

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gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
gcaggcccca acatcgccgc catcgtoggg ggcaccgtgg caggcatcgt gctgatcggc 2220
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ctcttgagga tgtcaccaat taaccagaaa tccagttatt ttccgccctc aaaatgacag 2520
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```

<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

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aggccagagt cttcccactg cccatgttcg cccttcccac ccattgaaga gcttcgccgt 120
gccagcaatc ccgctccag gacctccac ctatgatcct gcattgcaa gcacaccatt 180
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tctagggaa gggagccggc tcctatgcca gtggttggtt ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtgtt gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggagggatt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

gggcccgggc gggctgggct ggagcagcgg cgcccgggag ccgagcttgc agcgaggagc 60
cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgt 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactcctca gcacccctc 180
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tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagccttctc caaaaattga atggaaaaa gatggaactt ttttaaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

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cagccaacca gaaccttcct cagtttatgc tgggaacgga gcaattctga attgtgaagt 660
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ttctccctta gtcagagtca ttggtcagga tgtagtgt tg ccatgtgttg cttcaggact 960
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caaattgacg tggcgacac ctgcatcaga tccctacgga gacaacctta cctactctgt 1560
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tttggtagt ggtttaaagc cgaatacact ctatgaattc tctgtgatgg tgaccaaagg 2940
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cagggccaat tccacagaat ccgttcgaaa tccccagc actgacacca tgccagcctc 4080
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cttggccagc tccaagagg aagattcagg ccagagtctt ccca ctgccc atgttcgccc 4200
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aaaaaaaaa aaaaaaa 5297

```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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cagggaattn nttcatnatg gaaaagaca actgaatgcc ctcaactgaa tgtcttcac 60
ccctcttgcc tgaaatttcc accttcccat aggctgggga gggagtcagt tccagagcag 120
aggagggtga cagggttgag gagggacttg tgagagctag aacttgga aatggcctag 180
cccacccttc aaaggggaaa agagggagga acaggggatg aaaagtntc cgcagccttc 240
ccttgaaact tcccctgctg ggggagggag gaggttaaag caagaccccc tgcccagggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

```

<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

```

cgtcaacatg agttgggctt ggggcagatg aggctggctg gcggggcggg cagcatggtt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
ggtctggact ccccatcaga gcacacagac accgaaagaa atggacca ga cactaatcat 180
cagaaccccc aaaataagac ctccccattc tccgtgtccc caactggccc cagtacaaag 240
atcaaggctg aagaccccag tggcgattca gccccagcag caccctgcc ccctcagccg 300
gccccgcctc atctgccccg gcccactc atgttgacgg gcagccagct agctggggac 360
atacagcagc tcctccagct ccagca gctg gtgcttgtgc caggccacca cctccagcca 420
cctgctcagt tcctgctacc gcaggcccag cagagccagc caggcctgct accgacacca 480
aatctatttc agctacctca gcaaaccag ggagctcttc tgacctcca gccccggggc 540
gggcttcccc cacagcccc ccaatgcttg gagccaccat cccacccga ggagcccagt 600
gatctggagg agctggagca attcgccgc accttcaagc aacgccgat caagctgggc 660
ttcacgcagg gtgatgtggg cctggccatg ggcaagctct acggcaacga cttcagccag 720
acgaccattt cccgcttcga ggccctcaac ctgagcttca agaactgtg caaactcaag 780
cccctcctgg agaagtggct caacgatgca gagactatgt ctgtgg actc aagcctgcc 840
agccccaacc agctgagcag cccagcctg ggtttcgacg gcctgcccgg ccggagaccg 900
aagaagagga ccagcatcga gacaaacgct cgcttcgct tagagaagag ttttctagcg 960
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agaggggcag gaggccagt gtggggacgc agagggctct cagagcagga gtgacaagg 1860
aggaaagacc aaaaaaaca ccaacaaaa aaaaaaaa aaaaggaaa aaactaacca 1920
acaaaagaga aaacaaaaa taatcacaa agaaaccagc tgcccaaaag gaaccagagg 1980
tgaaaaacaa aaaaaaaa caaaaaaca accaaaaaa aaaaaaacc tctacccct 2040
ctagagcc 2048

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<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

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ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaaattatg 60
tgattgggga gattaactct aatctccaca tttatataca gaaagctoca ttgtttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gatttatatt ccaactaaaa cactgccatg tacatttttt ttctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

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<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
gaaaagggtg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
aaaacttgtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
gcagggtttc ttatactggg tgaaggagat accgtgcggt gcttt agttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
tgcagattta tcaacggcctt ttatcttgaa aatagtgcga cgcagtctac aaattctggt 360
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca tttgcctta 420
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcaggt tgtagatata 480
tcagacacca tatacccgag gaacctgcc atgtattgtg aagaagctag attaaagtc 540
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
tggaacactt gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttctt 720
gttttgggcc ggaatcttaa tattcgaagt gaatctgat ctgtgagttc tgataggaat 780
ttcccaaatt caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840
tttacttttg ggacatggat atactcagtt aacaaggagc agc ttgcaag agctggattt 900
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gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
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aagaaaataa tggaggaaaa aattcagata tctgggagca actataaato acttgagggt 1260
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tagcatttgc taccagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
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attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
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ttaaatgtgg ttctctctcg gggagggggg gattggggga ggggccccag aggggtttta 2340
gaggggcctt ttcactttcg acttttttca ttttgttctg ttcggatttt ttataagtat 2400
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ctgagtgtcg ggccactttg 2540

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<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gtttaggaa caagggaata tcttattgtc acgcattcac 120
agtgaacccc attttaatgc aggtccagag ccaactgcag tccgtgccaa tcccataggt 180
acaaggcctt ggctcctctt cctgtgtact gcccgacttc ctcattctac tgggtccagc 240
ataaagcaga tgtccactgt ctctct caca tgctgtgatc ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggttcgctt acttaggaac agcagctctt tttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaattcc tttgggttat agttggaac caggatggga ataaagggat ccagggcac 480
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cccagctctg ctcagagccg acacaatggc gcctccatgc caatcatnct tcatcatttt 600
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660
gagggttctt ccccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctcttttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgccctgtca aaccacttct cccagaagac tccctttctt aggtttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
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ctcactgtga aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120
ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgacct 240
ggccaagcat ggggatcagc acgagggtca gcacta caac atctccccc aggatttga 300
gactgtattt ccccatggcc ttcctcctcg ctttgtgatg cagggtgaaga cattcagtga 360
agcttgctg atggttaagga aaccagccct agaacttctg cattacctga aaaacaccag 420
tttgcttat ccagctatac gatattctt gtatggagag aagggaacag gaaaaaccct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgctcat ctttgggtga aaaattgtcg ggatcttctg cagtccagct acaacaaaca 600
gcgctttgat caacctttag aggtttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttctcg aaccagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720
tgagaaaggg agtctcttg gagaaagtg gtaacagggc ataacacggg tgaggaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
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agaagataaa agccccgattg cccccgagga atta gcactt gttcacaact tgaggaaaat 960
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ctttaagccc cggaagcct atctgccccca ggagttgctg ggaaaggaag gatttgatgc 1080
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gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcactgtgc 1260
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tgggattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcactgtgaa 1440
tgcgtgacaa taagatatcc cctgtttcct aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaaa 1608

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<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone). (GNRH1) gene.

<400> 277

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ttagattgca tgcatttgta tgcctacagg gcatttgaca gcccaaggnt aaatccagg 60
gggacgggat ctaatgatgt cctgtccttc actgtccttg ccaccaccag ccacagagat 120
ccaggctttg gggactocca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
actaggaagg catctggctc ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t

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<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

<400> 278

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gggatctttt tggctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

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ccttacacca agttgcacat attccataat aaagtgtgtg gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgaggggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240
gtatgagacg caggtgggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300
ctgggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaactttt cggcctggag tgggtgtgtt aagggactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attccccaa aaggaggggc 120
ccttgaggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180
tggtacacc taaagcctga aacctgaacc ccantactct gacagaagaa cccaggggtc 240
ctgtagccct aagtgggtact aactttcctt cattcaacc acctgcgtct tatactcanc 300
tcanccact gttggctgat tttggatttt tgtggcccca tgtaaggaac cctttaattt 360
ggcattnccc aattgagaat taaccttttt gncctgaaca tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe
combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttccctgcagc 60
tgccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
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tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 282
atctaacaca acactttaga aagatatattt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagt aaacccattt taatgcaggt ccagagccaa ctgcagtcct 180
gtccaatccc ataggttaca agggcctggg ctctcttcc tgtgtactgc ccgacttcc 240
catcttactg gggccagca taaagcagga tgcactgt ctctctcaca tgctgtganc 300
ttggncttag gagtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(358)

<223> 5' terminal sequence. death associated protein 3 (DAP3) gene.

<400> 283

aggacgggcg ctttgagacc ggccccaggc agcgtgtgtc ggtcgccctag tctggagaac 60
tagtcctcga ct cactgtga aggatgatgc tgaaaggaat aacaaggctt atctctagga 120
tccataagtt ggaccctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccca ggttcccagt tgagagtccc gagagctatt ttcccgaac 240
caatgagaat gaccccgccc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358

<210> 284

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 5' terminal sequence. ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 284

gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgcca aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctggttg aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt ttttgttttg ttttttttc aatcat 416

<210> 285

<211> 3052

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3052)

<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285

ccggtgtgaa ggccatgagt gattactggg ttgttggaag gaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttcctaagag tttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gcttcaagtg tgctcttggt tcaagctgga ttatttcagt ggaactggca atcggccag 300

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgcga aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgcg ggcaccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctcgagc 540
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ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
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gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaagg ggaatggcaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 286

gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctocata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcctcc 240
atgggcagcc actccattgc tcaactccgn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

<210> 287

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 287

catatctgga caaggcaccc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtggtna aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttgg 300
ctgtatcttt gcagagatgt ttcgtcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363

<210> 288

<211> 1443

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1443)

<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288

gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggctgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggccgtagga accggtccg gggccccgat aacggggccg 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttgggtgcgg tgcctatggg acagtgt aca agggccgtga 300
tcccacagt ggccactttg tggccctcaa gagtgtgaga gtcccgaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagtctg tgagggtgct ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca thtagaccag gacctaaagg catatctgga 540
caaggcaccc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagaggccta gatttccttc atgccaattg catcgttcac cgagatctga agccagagaa 660
cattctggtg acaagtgggt gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720

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cagctaccag atggcactta caccggtggt tgttacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggtggct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
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tgcttttoga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgcgc 1140
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gcaatctttg cctttatctc tgaggctatg gagggtcctc ctccatcttt ctacagagat 1260
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ttccatttc tctacactaa ggggtatgtt ccctctgtc cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

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<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

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ccgcggtgtg tgcgcctaan ctccgnggn ccacccgaga ccccttgagc accaaccccta 60
gtccccgcg cggccctna ttcgctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcagaaaa 180
gaagaagggtg gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttagggt gtaaacataa tctctggnat tgaagagggtg aatatgttta caaacagggt 300
aacagtgtac cactttaaca acc tnaagt tcagggtcgc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaagcag ctgg 394

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<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

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atgcgacgga caggcgcacc cgctcaggct gactctcggg ggcgaggctg agccaggggc 60
ggctgccctg gggcgaggc gacgctgtct caacctccac ctgcggcgag aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg tttaaaacc aaggaacagt gatccacttt 240
aacaacccta agttcaggc atctctggca ggaacactt tcaccattac aggccatgct 300
gagacaaaag agctgcagaa aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgcccaaac aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

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<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tcctgcttgg ngtgggccagc cacatgccaa ggtcccctgc 120
cttctagccc agaatgacgg gactgggcag aacaccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttgagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attcttagag gagccatcct gntccaaggg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctcagagagg ggagatctca 360
ctctctgcca gtctgtctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v-fms)
oncogene homolog (CSF1R) gene.

<400> 292
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
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cgatgtgtgg gcaatggcag cgtggaatgg gatggcccc catcacctca ctggaccctg 480
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cgggactata ccaatctgcc gagcagcagc agaagcgggt gcagcggcag cagcagcagt 3120
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tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctacggcccc ttggagcagg atggctcctc taag aatctc 3720
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ccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg ggtgttctgc 3840
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caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
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```

<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature
<222> (1)..(356)
<223> 3' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 293
tttatttagt caaattattt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
aatatagtta aaaaagtcaa caattacctg caaaattata tataatntnaa tgtctaaaaa 120
tatgtngctt atatatagca ggaaaatccc tctctccac aagggaagt ttcgttggtt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240
aatgggatta tcttttncct gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggtata g ggcatt 356

<210> 294
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 294
gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgctcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaagaa ggtt tgtgtg tttaagacgc caagggcatt 240
gcagaatccc tctcagtgga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
attaaattna ctaattttnt tttttttttt ttaaattgatn gacagtggnt ccccggaact 420
tgggaaangt tgtaggggnt ttctaaaccc aagncgattc gcant 465

<210> 295
<211> 2957
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2957)
<223> friend leukemia virus integrati on 1 (FLI1)
gene.

<400> 295
gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60
ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120
taaccgggtc aatgtgtgga atattggggg gctcggctgc agacttggcc aaatggacgg 180
gactattaag gaggctctgt cggtggtgag cgacgaccag tccctctttg actcagcgta 240
cggagcggca gccatctctc ccaaggccga catgactgcc tcggggagtc ctgactacgg 300
gcagcccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagtga 360
ggtcaacgctc aagcggggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

192/292

```

cagcgttagc aaatgcagca agctgggtggg cggaggcgag tccaaccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtggggccata aaggagtaca gcttgatgga gatcgacaca tcctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgtgtgcac acctcagtta cctcaggga agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
cctcatcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtccctc 900
ccttgagggg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccgacca gcagtgcct agccaacct ggaagcgggc agatccagct 1020
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cggcattgac caggctctgc agc cacatcc gaccgagtcg tccatgtaca agtacccttc 1320
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cgtgccttca cacttaggca gctactacta gaagcttctt ctagtgaag cccatcctgc 1560
acacttactg gatgcttttg actcaacagg acatatgtgg ccttgaaggg aagacaaaac 1620
tggatgttct ttctgtttg atagaacctt tgtatgtgt ctttaaaaac atttttttta 1680
atgttggtaa cttttgcttc ctctacctga acaaaga gat gaataattcc atgggccagt 1740
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atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaataca cggggttcag tatgacacag aatcatggac ttaaccogtc 1920
atgttctggt ttgagattta gtgacaaata gagtgaggaa gcttataatc taatttttagg 1980
aggaccaaat tcagcggatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
ccaactggaa ttgatggaa agaaggtttg tgtgtttaag acgccaaggg cattgcagaa 2100
tccctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaatgc aaatacatac attcctgaaa gacggggaat taaattacta 2220
attttttttt tttaaatgat gacagtggtc ccagaacttg gaaaagttgt agggatttct 2280
aaactcaagc agattcgcaa gtgctgtgcg cttgtcagac catcagacca gggccaacca 2340
atcagaaggc aacttactgt ataaa ttatg cagagttatt ttcctatatc tcacagtatt 2400
aaaaaataaa taattaaaaa ttaagaataa ataaacgagt tgacctcggc cacaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaag taatttgtac atcttttttc 2520
aatctgtaca tttgggctgt cttgtatgtt tttatgctcc tttttaaaaa gcataatatg 2580
cctatagctg aaaaggaac agggctgttt aagtactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaa cagggaagaa ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata tttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

```

<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```
caccccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc cctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttgttttt tgttttttta gatacaaatc ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400
```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```
cgtggtagat tttcatagt cgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gtttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgtctatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaatggta 180
tgcactcaat aaatatTTTT ggaatgaatt aaagagtggc atggccttaca gaagtataga 240
tgtagtata gtatccgtt gagcctttgc tttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca ctgacctgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacctct atggcctcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464
```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

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aaataccaaa actacaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaataaaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccctt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaatgggt 360
tnaggcctcc ccaacttt 378
```

<210> 299

<211> 317

194/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga cccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtcggttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccaactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

```
gagtcagacc gctggtgcgc ggagcgggtc accgtcttcg gagcgggttcg gccagccctt 60
tcgccaggcc gccaggcccc gctgcgcgcg tgcgtgagcg cgcctgcgcc gccaggggccg 120
ctgcaagggg aggagagcgg ccgcctcagg aggatccctt ttccccaga aattactcaa 180
tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ctttttatgg tcccaggga atctcgatct gaggaatgca gagggcggcc 300
tgtgattgac agaaagagga agtttttga cacagatctg gctcacgatt ctgaagagct 360
atttcaggat ctcaagtcaac ttcaagaggc ttgggttagct gaagcacaag ttcctgatga 420
tgaacagttt gtccagatt ttcaagtctga taacctggtg ctcatgccc cacctccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tccatacaacc cccctctcac ccacccatca 660
gaatccccta ttccccccac ctcaaggcaac tctgccacc tcagggcagtg cccctgcagc 720
tgcccagtt caaggtgtgg gcccgcgcc cgccccccat tcgcttcagc agcctggacc 780
acagcagcaa acatttgcg tcccccgacc accacatcag cccctgcaga tgccaaagat 840
gatgcctgaa aaccagtatc catcagaaca gagatttc ag agacaactgt ctgaaccctg 900
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cattgcctgg acaggtcgag gcatggagtt caagctgata gaaccggaag aggttgctcg 1440
gcgtgggggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
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195/292

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ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
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cctgaaggca gagtccgagt gccacctcag cgaggaggac accctgccgc tgaccactt 1680
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cattggctgg ggagtgggaa cagggagggg cagaaaacca c caaaaggcc agtgcctcaa 1980
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atctcgatcg atcatggact actaaatggc cttacatag aagggctctg atttgacaa 2160
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cttgcccatg tgaagcccg ccttgttgcc tgctttgtgc ttctgcacc agacaacctg 2760
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aattattctc attgctgtat tatattggaa aagttttaaa caaccaagct aaagctatgt 3180
gaaagttgag ctcaaagtag aggaaaagt actggtggta ccttgcctgc tgctctgctg 3240
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gaacctgcca gctgatttga aatactttca ccctgcgcag ggcgctatgc atcctgcca 4020
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```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

```

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

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196/292

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagnataa ggcaaagntt gccctctcag tntcngaag ggaaatggca gcttttcttc 240
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gggtgctgca gagctcgaaa ggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
ncccgacgca gctttgcttc cccgactcct nccttttcag gnacccc 407

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

attcgnaca gaggaggagg tggaggaggc cttccatca gcacagtctg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaatg catcggtcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaaata 60
ttaagttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatattaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa ggtaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccgccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

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```


198/292

```

gttatggctt cacatcoatt gcagtgggat atgggttttta tgtaaaacat ttttagaact 3120
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gagtcctcgt ctgccgccca ggctggagtg cagtggcgcg atctcggctc actgcaagct 3240
ctgcctccca ggttcacacc attctcctgc ctcagcctcc cgagtagctg ggactacagg 3300
tgcccaccac cagcctgggc tagttttttg tatttttagt agagacgcag tttcaccgtg 3360
ttagccagga tggctctgat ctcttgacct tgtgatctgc ccgcctcggc ctcccaaagt 3420
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tattcatttt aaattgttct gtatttttaa attgccaaga aaaacaactt tgtaaatgtg 4320
gagatatttt ccaacagctt ttctgtctta gtgtcttaat gtggaagtta acccttacca 4380
aaaaaggaag ttggcaaaaa cagccttcta gcacactttt ttaaatgaat aatggtagcc 4440
taaacttaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
ttctcattga atgcacc 4517

```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced protein 75, 52kd (IFI75) gene.

<400> 305

```

ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcagggttg cactggccac ttgcacagtg ctagtgagga 180
ggctgggcat ctctcttgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
tcactgaagt gcttcttctt tcctgggatg agtgcaggga gaggcaggac agggtcagat 300
gggctgggcy actcaactcg gatctcatcg ctttctggg agg atgttcc agggctcact 360
gactcttggg cgcacaaggt gaaacagctt ggtttgaagg gggtnnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttccct ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga ctctctgttt tgcctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttaccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgcc atgccatata caagccatit cccttctttg aaggcctcct 240
agacaactcc atcatcata agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctcacccaa ctgggagagg actttttaac 360
ctgtntctctt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon -induced protein 75, 52kd (IFI75)
gene.

<400> 307
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tgaacagctt ggttgagtcg cccagcccat ctgacctgt cctgcctctc cctgcactca 120
tccaggaagg agaagcact tcagtgacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tccactagcac tgtgcaagtg gccagtga 240
acctgatccc ccaaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaaccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctgttcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggggtggatc aggttcctca aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaaa aggcgagAAC tgaatgtgcc cgaaagtcca 600
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660
cgcctagtac accacgaagg gtcacacaag ggcagcctc acctgggcat ggcattccaag 720
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aggtcatgat gagggtccaa aaggcaagaa ctaaatgtgc ccgaaagtcc agatcgaaag 840
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aaggaaaggaa cgaaagaac tggaaacgga atatacgttg tgaaggaaag accctaggag 1140
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atttaatatc cgagattacg gtgagccttt caggaagcaa tgtggttggg cctggttaag 1500
ggaaaggctg attacggaaa tgtacacggt ggcccggaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

```

gttannnnan tnnatttttt aagagagagg caatttttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctgggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416

```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

```

gaactcatc tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggaccatt caagaaagtc cggaaagtctc tggctcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc ccttcaaact 180
cttccagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggttct 240
tgcaggccaa gcccagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgccctat gtccagtgc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426

```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

<400> 310

```

gctgacgcct tgcagcgcgg ccc ggggccc ggagcggccg gagcagcccg ggtcctgacc 60
cgggcccggc tcccgcctccg ggctctgccg gcgggcccggc gagcgcggcg cgggccgggc 120
cgggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcact accaggacac 180
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ggacgagcag ctgaggggccc tggtaggca gtttgacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
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taagaagtat ggcacaaagc agtggacact gattgccaa cacc tgaagg gccggtggg 480
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gcctcatctc agaccctgct taggatggg gatgtggcca ggggtgctcc tgtgctcacc 2580
ctctcttggg gcattttttt ggaagaataa aattgcctct ctctttg 2627

```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth
factor, beta receptor iii (betaglyc an, 300kd)

202/292

(TGFB3) gene.

<400> 311

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cccagactca aggagttggt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa tttgcacott tgtctggatg cacacttctg acctgtctgc 180
cacaacctgt ggggttctga tgtgtccott gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt cccatacttg catacaccac tggcaaatg tottaatggc 360
aaattttgta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggcccatt tc                                         442
```

<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

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taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt tttccaatct cagcactgtc ttgngngaag 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta                                         315
```

<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

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tctttaagat ttgtagctac taagaaagaa aggagctttt tttccttggg cttcaaact 60
gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga cttaagact acttctgatt tgcaaagatg gtctgtgctc 300
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tatgtgattg ccatctttgc cctgatgagc ttctgtttag cca ctgcagg tccagagcct 420
ggtgcactgt gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagc agaggcacia ctgggctgcc acaggagggtg 540
```

203/292

catgtcctga atctcgcact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
cacctgaatc ccatctcctc a gtccacatc caccacaagt ctgttgtgtt cctgctcaac 660
tccccacacc cctcgggtgtg gcacatgaag acagagagac ttgccactgg ggtctccaga 720
ctgttttttg tgctctgagg ttctgtggtc cagttttcat cagcaaactt ctcttgaca 780
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aaagtggggg aagatcaagt gtccctcca aagtgaaca tagggaagaa tttctctca 960
ctcaattacc ttgttgagta cttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
cagccccaga atgaggaagt acacatcacc gagctaatca ccccaactc taaccctac 1080
agtgttttcc aggtggatat aacaattgat ataagacctt ctcaagagga tcttgaagt 1140
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ttacttctct tgccttaaat atatcccata tatttaatat gtcaaaaagg gcttgagggtg 4140
aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtataacc 4200

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tccttggt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence.. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacctt tccctaatac ttnatnggtn acctctaggc ctgtgtgcgg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggtctaggc cctccagggt ccatactgt ggagtttggg ggggcaggtc tggcctttcc 180
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agtcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tccagccagc gggacaaant 360
ttcccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcgggt gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggctctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttaaccac ctggcttggg tcaacacccc ccggaagag 240
ggaggcttgg gccccctgaa catc ccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

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<221> misc_feature
<222> (1)..(937)
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316
cgcgccccca gggctcactt ggcgctgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagcccctga cttcaaggcc acagcgggtg ttgatggcgc cttcaaagag gtgaagctgt 180
cggactacaa agggaagtac gtggtcctct ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtcggg cgtctcgggtg gactc tcagt tcaccacact ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc cccttgaaca tccccctgct tgctgacgtg accagacgct 420
tgtctgagga ttacggcgtg ctgaaaaacg atgagggcac tgcttacagg ggcctcttta 480
tcatcgatgg caagggtgtc cttcgccaga tcaactgtta tgatttgctt gtgggacgct 540
ccgtggatga ggcctcgcgg ctggtccagg ccttccagta cacagacgag catggggaag 600
tttgtccggc tgcttgaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatattt ctccaaacac aattaggctg gctaacggat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacactgg gtgcc ctatg ctgaccagg 780
aaaggccaga cctgcccctc caaaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgccctc ccccaagccc acccagccgc 900
acacaggcct agaggtaacc aataaagtat tagggcc 937

<210> 317
<211> 451
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(451)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gcccgctccg tgccagacat ggacctatct gggctccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcact ccggtggtca cctgtactec cagctgcaact gctta cacgt 240
cttccttcgt cttacactac cccgaggctg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctct tgactcgttc agctnaccga cgggtcgtggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgccca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451

<210> 318
<211> 2084
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2084)
<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.

<400> 318

```

aaccgcatct gcagcgagca actgagaagc caagactgag ccggcggccg cggcgagcag 60
aacgagcagt gaccgtgctc ctacccagct ctgcttcaca gcgcccacct gtctccgccc 120
ctcgcccccct cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgagcg gtcatactcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240
actaccactc acccgagac tccttctcca gcatgggctc gcctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtgcc aattcattcc caccgtcact gccatctcga 360
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agaccagagc ccctcaccct ttccggagtc ccgccccctc cgctggggct tactccaggg 480
ctggcggtgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaaggaa aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atctggcag ctaccgacc tgctgcaag atccctgatg 780
acctgggctt ccagaaagag atgtctgtgg ctcccttga tctgactggg ggcctgccag 840
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ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
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gctccctggg gatggggccc atggccacag agctggagcc cctgtgact ccggtgggta 1140
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gtgggcctca aggacttgaa agcatccatg tgtggactca agtccttacc tctccggag 1500
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agtagcatgt tgagccaggc ctgggtctgt gtctctttt tctttctcct tagtctctc 1620
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gaaataaata gctatatoca tgtactgtag ttttcttca acatcaatgt tcattgtaat 1860
gttactgac atgcattgtt gaggtggtct gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt tttctacct tgaggctctt tgacatgtgg aaagtgaatt tgaatgaaa 2040
atthaagcat tgtttgctta ttgtccaag acattgtcaa taaa 2084

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<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

```

ctgcaaagcc aatcaagaag tgttgaagg aaaaagtgtg aaagttatct ttgcataatt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cttctctctc 180
ttccctaata gctacaatnt gatacagtac gcaacagctc acttgaaagt gctagantca 240

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<210> 320

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<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 320
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
agaatacacc gtttctatat gacctggtta tgacccatgc tcttcagtgg cccagtctta 120
ccgttcagtg gtttcttgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggcttttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctcgtt aacatggcgc cagantcctt cacatccatt gttacaaan 420
acaccctctt gcttgatggt gttggnnttt tgactat 457

<210> 321
<211> 1946
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1946)
<223> retinoblastoma -binding protein 7 (RBBP7)
gene.

<400> 321
gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctcagacctc ggtacccgcg agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc tttcgacagt 180
ggggagtgtg acgcgcttgg gaaaggcagg agcgcacgcg gtcgggctgc tcttggttaa 240
cgagaggagt ccgaggcggc ggcgaggggc gaacgacccg acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360
agaatacacc gtttctatat gacctggtta tgacccatgc tcttcagtgg cccagtctta 420
ccgttcagtg gtttcttgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtggttgct cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggcttttg ttctgtaaca ggaanaattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttggttttt gactatacaa aacaccctgc taaaccagac ccaagtggag 780
aattgaaatc ttgatctcaga ttaagaggtc accagaagga aggctatggt ctctcctgga 840
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gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcatccaat ccctacagcg 1140
aatttattct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaatttaa actccatacc ttogaatctc ataaagatga aattttccag gtccactggt 1260
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgcctg aatgtgtggg 1320

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atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aacccaatg 1440
agccttgggt catttgc tca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccga aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtgggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagt agctgttgcg tactgtatca tattgtagct 1740
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agcaggtat tgcctttgat tcaactgttt taagtctca ttttctcaaa ctaagtgcct 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaat 1946

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<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

```

tatagaaatt ctttattatt agacaaaaat agactctctt ttttcccta ttcattgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccacccct ctcccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgattccct gggagggctg 180
acgttctcct gcaggtgggg ctgctgctgc tccttcgggg ctcaactgct gatgcctcct 240
caccctcac acaccatct ctgccatctg ctccatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365

```

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

```

tcaagggtg cccagtgag ccctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctccctg ccctgctgcc tgcgattcc cagcaaagat cctctggaag 120
agaccccaga ggtccagtg cccaccaaca tgagcacagc gncagacctc ctgctcagg 180
gtgctgcctg caggtngctc tacttgacct cagtggagac agagtcactg acggggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g cccccgccg acaccagctg 300
ttgtccactt caaggtgtca gccagggca ttacactga cgggacaacc aaaggaagct 360
ctttnttttc gccgccatta tccagtggaa cagcatcacc 400

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<210> 324
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 5' terminal sequence. atp-binding cassette,
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
nttcggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60
attcttccca gcacgcacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120
agcgcagagg atcagccttg cccgggcctt gtatagtac aggagcatct acatcctgga 180
cgacccctc agtgoccttag atgcccattg ggaanccaca tncctcaata gtgctatccg 240
gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300
actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcaccntg 360
gaggaantg atggatttta aatgggtgatt atggttacct ttttaattaa cntgtgttg 420
ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
ttcacagtt 489

<210> 325
<211> 5838
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5838)
<223> atp-binding cassette, sub-family c
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325
ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcggtt gtcctggagc 60
aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
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<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

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385

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<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

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<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
(CDH1) gene.

<400> 328

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<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

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<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

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gccaccacc ctacctccc cactccccct tcgacagcca gtggggccac c acagctgcc 1140
aacgggggta gcttgaactg cctgcagaca ccactctcca ccagcagggg gcgcaagatg 1200
actgtcaacg gcgtcccggt gcccccctta acttgaggcc agggaccctc tcccttcttc 1260
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tccccagctc tccccacctt ggggggt gggg ggcgggtttt ataaataaat atatatatat 1380
atgtacatag gaaaaacaa atatacatat ttattttcta tggaccaacc agattaattt 1440
aaatgccaca ggaacaaaac tttatgtgtg tgtgtatgtg tggaaaatgg tgttcatttt 1500
ttttgggggg ggtcttgtgt aatttgctgt ttttgggggt gcctggagat gaactggatg 1560
ggccaactga gtctcaataa agctctgcac catcctcgct gtttcccaag gcagtggtg 1620
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ttttacaaat gcagtttatc cctggttctg agggcaagt gcagggtgga ggtggcacct 1860
gcatacctc ctctcttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920
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aggccctgag aggtctcagc tcttgaggga gggctaaggc ttttagcattg tgaagcgctg 2040
caccctcacc aaccttacc tcaccgggga accctacta gcaggactgg tggaggagtc 2100
tcacctgggg cctagagtgg aagtgggggt gggttaacct cacacaagca cagatcccag 2160
actttgccag aggcaaacag ggaattccgc cgatactgac gggctccagg agt cgtcgcc 2220
acactcg 2227
```

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(254)

<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180
tccttcagg gaccagcag ttgtgggtaa agcaggcaag tgggccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
gccatggnc tggtgctaca cgatggaccc aaggacccca t tcgactact gtgccctgog 60
acgtgcgct gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagaggttg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
tgcggngngt ctctagttaa ggagcagtn atactgactn cccggaagtg cttctcctcc 300
tnccatatnc ctctcaggg ctatgaggta tggtingggc ancctttttc cagaaccac 360
ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2219)

<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

216/292

<400> 333

```
agccagaagg atgggggtggc tccactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct 120
gctacatgcg gtgggtgccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg 240
ttgccaaactg ctgccatgga ctcaacactc gcccacacg aggctgcggc gttctggggc 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg 360
gtaccggggc accatggcca cgaccgtggg tggcctgcc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggcttgaag agaacttctg 480
ccgtaaccct gatggcgac c cggaggtcc ttgggtgtac acaacagacc ctgtgtgctg 540
cttccagagc tgcggcatca aatcctgccg ggaggccggc tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcggtag accgcacgga gtcaggcgcg gactgccagc gctgggatct 660
tcagcaccgc caccagcacc ccttcgagcc gggcaagtcc ctcgaccaag gctctggacga 720
caactattgc cggaaatctg acggctccga cgggccatgg tgctacacta cggatccgca 780
gatcgagcga gagttctgtg acctcccccg ctgcgggtcc gaggcacagc cccgccaa 840
ggccacaact gtcagctgct tccgcgggaa gggtagggc taccggggca cagccaatac 900
caccactgcg ggcgtacctt gccagcgttg ggacgcga a atccgcctc agcaccgatt 960
tacgccagaa aaatacgcgt gcaaagacct tcgggagaac ttctgccgga accccgacgg 1020
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gacgcgcgac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgccgg aaccagatg gggatagcca tggccctgg tgctacacga tggaccaag 1320
gaccccatc gactactgtg cctgcgcagc ctgcgtgat gaccagccgc cat caatcct 1380
ggacccccca gaccaggtgc agtttgagaa gtgtggcaag aggttgatc ggctggatca 1440
cggcgcttcc aagctgcgcg tggttggggg ccatccgggc aactcaccct ggacagtcag 1500
cttcgggaat cggcagggcc agcatttctg cggggggtct ctagtgaagg agcagtggt 1560
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gttgggcacc ctgttccaga accacagca tggagagcca agcctacagc gggctccagt 1680
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tgtgacctg aaccagcgtg tggccctgat ctgcctgccc cctgaatggt atgtggtgcc 1800
tocagggacc aagtgtgaga ttgcaggctg gggtagacc aaaggtagcg gtaatgacac 1860
agtcctaaat gtggccttcc tgaatgttat ctccaaccag gactgtaaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccctg tgggggcctg 1980
tgagggtgac tacggggggc cacttgctg ctttaccac a actgctggg tcttggagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgctg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggt catgagactg ggttaggcc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219
```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```
gaaaggaagg caaactctgc ccccc gctca gactcccccc aaccctcaact gtttcccggt 60
gccattgatg gggagggttca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcacacat atgctgagag caggggggaa gcacccaggc agccagggt 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggtctcaa aaggcttcag 300
```

217/292

ttgcccgggc agtgccttca catagtcac cttgcccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggtg 420
nctccntttt t 431

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335
nattcggcac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccacctgcg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336
ggagtttcgc cgcgcagtc ttcgccacca tgccgccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgetggcaga tcagg gccag agctggaagg 120
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatac 180
ggcagctccc caagttccag gacggagacc tcaccctgta ccagtccaat accatcctgc 240
gtcacctggg cgcaccctt gggtctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaac caggagggca agacctcat tgtgggagac cagatctcct 480
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tggatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgcccg cccaagctca 600
aggccttcct ggcctccct gagtacgtga acctcccat caatggcaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gaggttgcct tcctttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaagggtcaaa ccaccataga 60
tttgaatctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tcnngggttt ttcttagggt aggctgagga ctcaggggct tatctcacct tctcaggaat 360
gctttttgaa gg                                     372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtaacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatoctct ggaacttgag 180
gaagtgaaca tttcgggtgac ttccgcatca ggaaggctag agttaccagc agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtocctggga ctgagccggg gccctcactg gccttcttc caggggatgg 360
atcaacaggg gcagtgtggt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcccttttt aagtggga                                     508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```
tttttttant caaaagtttg aaattcaagt aactttattt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctagggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antagggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcaggtata tgctgggcât cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt gggggnggcc aggtaggtn tttagggtgc cccntatccc 420
ganttttata ctctncaccg ggggg                                     445
```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```
gctccagcgt tgtaaacctg cagagatgga ctggtccac gtctctttgg tgcagctcac 60
cctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tgggggaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatgac cttggcgcta gtatttgaag caccaaacca ggagaaagt 240
tcagactatg aaatgaagt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgcntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact                                     437
```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```
aggtctcagc cggctcgtgc gacgttcgcc cgctcgtct gaggtcctg aagccgaaac 60
tagctagact ttctctcttc ccgctgcct gtacggcgt tgttgccact ccgccaccat 120
gttcgaggcg cgctgggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctcgtccac gtctctttgg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttacactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggatgaatt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660
```

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaagaat 1080
aaagtcacaa gtctgatctg gtctagttaa cctagaagta tttttgtctc tttagaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c                                     1231

```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5' el
binding protein (BS69) gene.

<400> 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aaggttaagt gttctcggtt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac                                     383

```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5' el
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcatct ttgtcctaac atgagtgtt gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt cccttcctt ccacatatc atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttaggtt aatgggggtc ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggtctg gtattttgcg gggatgtctg gggttaggga ggccttacc ataggggntg 480
ggg                                     483

```

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaagaag taaacaggtc atggcacgtt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaaacat tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggg 180
gattttttaca tcattacaca gatatgtcat ttctattagt tgtatcattg ttataaactg 240
gtatatgtct cgagtccacg gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggtt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaaatca 420
tgactgggtat tgttttgaat gccatttgcc tggagagggtg ttgatattgtg acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagtccagg cttagagaca gcagtagtcc 540
ctggcagtgcc ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600
cacataacctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggctgggt cactcagctg tggacgttcc 720
caccattcaa gagaaagtga atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780
tgcccaattg cttctccaca ataccgtgat ttctatgga gcagacagtg agcaagctga 840
cattgacgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaaagaa gacaatcaag tgcacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtgc acgtgaagcg 1140
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
agggagattt tggaaatcta agaagtagga ccgaggtgag gaagaggcag aatccagtat 1260
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acgtaatcaa agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaataccca cgatgcctca gcc atcgaa aaagtctccg tgtaactca 1440
gacaaagaag ttaagtgcct cttaccaag aatgctgcat cggagcacc agaccacaaa 1500
cgacggcgtg tgtcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560
agaccggtg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctcgt tctgaaatgg aagaagaaaa gagacaagct gtaaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740
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gaagcagtg tgcacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920
ccgaaaaaga tgaagctggc ccttcccgga gtcaccccgga tgattactct tttcagacac 1980
agcgtttttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcaggggg taaaagttaac atcagtggag ggtattatct taaataaatt 2160
ttaattgaga atttgttgca ttttcagcaa attttaaaac atttttaggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa aacagggtgaa tacaagttag tttacaaaag 2 280
aaacatttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
ctgttcaaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460
gggttgacac agcagggtc gtcctgcata tttttt ctta aatattttcc aattgtgttt 2520
ttcattatct cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580
ttaaaattgc agggaaactg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640
tttaaatctt aaagtgtgcc acatttcac tttgtcctaa catgagtgtc tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix
metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcattgcagca tcttgagtgg tagcgtcgat ctacagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccc ggtgctgggg tggaaacgcc agtagtcctc 120
gcctcggaag aagtagatct tggtcttctc gggaccccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttgga agaaccaaat gtgggcccgg cttaccacgc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca
```

363

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gccccggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgctgctgct gctccagccg ccgcccgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agcctgccc agtagcccg caccctgccc tgccacgcag gaagccccc ggccctgccag 240
cagcctcagg cctcccgcgt gtggcggtgc cgaccatct gatgggctga gtgcccga 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gatccttcgg ttcccatggc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttcg ccaggctactg ccattggggac gacctgccgt ttgatgggcc 540
tgggggcctc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcaggtggc 660
agcccatgaa tttggccacg tgctggggct gcagcacaca acagcagcca aggcctgat 720
gtccgccttc tacaccttcc gctaccact gagtctcagc ccagatgact gcagggcgct 780
tcaacaccta tatggccagc cctggccccc tgtcacctcc aggaccccag ccctgggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cgggtctccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgccctc gtggggggcca gctgcagccc ggctaccagc cattggcctc 1020
tcgccactgg cagggactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttccaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```
ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccgag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccogg cgtgtagaca gtcccggtgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc ccggtctcgt 1440
gggtcctgac ttctttggct gtgccgagcc tgccaacact ttctctgac catggcttgg 1500
atgccctcag ggggtgctgac cctgcccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg caggagggtt ttggcatgac tt aagaggaa gggcagtctt 1740
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gtagcaccat ggcaggactg ggggaactgg agtgtccttg ctgtatccct gttgtgaggt 1860
tccttccagg ggtggcact gaagcaagg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggtgta ggg cagggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggttattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260
```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```
atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaaggtagg tgttacgaat 180
catcggggct gtggccagnt tgcctcacgg aggtgcaggg aggtgagggc ctcactaggg 240
canctggagg agcacggact gccctgccgg cag 273
```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```
ggagtacaga acattgtggt aggggaaggg actcacttcc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180
```

224/292

```

cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagccngg tgaagnacca                               330

```

<210> 349

<211> 1168

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prime r

<220>

<221> misc_feature

<222> (1)..(1168)

<223> hypothetical protein mgc13071 (MGC13071)
gene.

<400> 349

```

aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggectggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgtttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag ctctctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tctcaagtc actggtggct cgctttgatg ctggagaact aatcaccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctctattctg 600
acgacgtgtc tttagacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgagggtga 720
ctccaaggca gctgagctga tcgccaaetc actggccact gcaggggacg gccagagcga 7 80
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtcctgtct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgttaaca ccacctttcg 960
ccctcacccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168

```

<210> 350

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. interleukin enhancer
binding factor 2, 45kd (ILF2) gene.

<400> 350

```

ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggttc gaggaaatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240

```

225/292

cccnggatnc ttgaactact aggn cattat gctgtgatga acaacccac caganagcct 300
 ttggcnctaa acgtt 315

<210> 351
 <211> 1552
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1552)
 <223> interleukin enhancer binding factor 2, 45kd
 (ILF2) gene.

<400> 351
 cgggttggtgc ggcctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
 ggtcgtggtg ggcgcttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
 ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180
 cctgatgaaa cttccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
 tctgctgaac aggcattctat cctttctctg gtgacaaaaa taaacaatgt gattgataat 300
 ctgattgtgg ctccagggac a tttgaagt gaaattgaag aagttcgaca ggtgggatcc 360
 tataaaaagg ggacaatgac tacaggacac aatgtggctg acctggtggt gatactcaag 420
 attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
 gcacaggatc cttctgaagt ttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
 tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600
 gatccagaac tccatttgga tatcaaagta ttgcagagt gcttagcagc catccgacat 660
 gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
 aaggacttga ggattcggtt tcttggtctt gagccctca c acctggat ccttgaccta 780
 ctaggccatt atgctgtgat gaacaacccc accagacagc ctttgccct aaacgttgca 840
 tacaggcgct gcttgcatg tctggctgca ggactgttc tgccagggtc agtgggtatc 900
 actgaccct gtgagagtgg caactttaga gtacacacag tcatgacct agaacagcag 960
 gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020
 aagatccttg gccaggagg tgatgccagc tatcttgct ctgaaatata tacctgggat 1080
 ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
 gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
 aactcaggag tgacattccc ttcactcctt ttcctaccca agggaaagac tggagcctaa 1260
 gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320
 aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
 tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
 taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500
 aatgttaagt gtctggaaat tttttttct aagaaaaact attaaagtac tt 1552

<210> 352
 <211> 396
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(396)
 <223> 3' terminal sequence. hypothetical protein
 flj11307 (FLJ11307) gene.

226/292

<400> 352

ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
gggtactggag gtttcagttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcac 180
aaagcctgtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

tcgatgaaag atcctccgga cttattggac aggcagaaat gcccgaacgc cttggcgtct 60
cttcgacatg ccaaattggtt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120
ctccgcatte tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggcccttga gacgagtaat ggagtggttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagacca acag atgctc tgagctatat gaccatccag 360
caaaaagaag atattacca cagtgcacag catgcaactc gactatcagc ctttggccag 420
atttacaaag tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc ccggttcagc cccagctctt cacaatgtct 720
gtagatgttg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780
cacgtagcgg tgaagggtatt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaaccctg taatggagct caatgaaaaa 1020
agaagagggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgcttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg caggteccaa taagaaagtg 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaaggcg tigtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctggcc ctgcttatgg tttacccaag agaattggtc tgttac ccgt tatgaaattt 1440
ccaacatate ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgac acaataaac tgctttgtt taacacag 1858

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaacccag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                     242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene
homolog (MYB) gene.

<400> 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggggggc agcggggaggc 60
ggcaccccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccccg gcacagcata tatagcagtg acgaggatga ttaggacttt gagatgtgtg 180
accatgacta tgatgggctg cttccaagt ctggaaagcg tcaacttggg aaaacaagggt 240
ggacccggga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaagttaa tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccttggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacggtccga aacgttgggc tgttattgcc aagcacttaa 480
aggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaaagtac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgctcgaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatggggt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagccact gttacaacag 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcagtgt ccataccctg 900
tagcggtaca tgtaaatata gtcaatgtcc ctgagccagc tgccgcagcc attcagagac 960
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tgtcaaccga gaatgagcta aaaggacagc aggtgtctacc aacacagaac cacacatgca 1080
gctaccccg gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagt 1140
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tggaataatg taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaat gccttcttta acttccaccc 1380
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ctcaagaac tcctacacca ttcaaacatg cacttgacg tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttggtg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatattctt acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcatacct gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcat tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgtggt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gattttttaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctgggtatttt 2340
aaaggatcca acagatcagt attttttcct gtgatgggtt ttttgaaatt tgacacatta 2400
aaaggtactc cagtatttca cttttctcga tcactaaaca tatgcatata tttttaaaaa 2460
tcagtaaaag cattactcta agtgtagact taataccatg tgacatttaa tccagattgt 2520
aaatgctcat ttatggttaa tgacattgaa ggtacattta ttgtaccaa ccattttatg 2580
agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
tatttttatt cagtaattta attttgtaaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggctcttagc ttagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgttaggt aattgactat gcaactagat ttcagacttt ttaattttat 2820
atatatatac atttttttcc cttctgcaat acatttgaaa acttgtttgg gagactctgc 2880
attttttatt gtggtttttt tgttattgtt gggtttatac agcatgcgtt gcacttcttt 2940
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ataatttggg agttctcgat ttgatccgca tcccctgtgg tttctaagtg tatggtctca 3060
gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

```

gtagttaaat gcagaaagtc ggttttttcc cacccttttc ctccttttac acggcaagta 60
aagctcactg gcctgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccttgact cgccacagcg gtaacagttg 240
acttcacttg tcttgctgca gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgagtccttt tttgaatgtg tcccgaattc tcccacaaga atancctttc 360
tgctcanct 369

```

<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
nucleic acid binding protein) (ZNF9) gene.

<400> 357
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggctgcgtc cgagtctccg 60
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccactgggccc cgggaatgtc ctactgggtg aggccgtggt 180
cgtggaatga gaagccgtgg cagaggtggt ttacctcgg atagaggttt ccagtttggt 240
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctgggtcatct tgccaaggat 300
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgctgctaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttggtg agaattcgga 480
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tgggtcatgta 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcaggggcac 600
cttgacaggg aatgcacaat tgaggctaca gcctaattat ttcccttgt cgccctcct 660
ttttctgatt gatggttgta ttattttctc tgaatcctct tcaactggcca aaggttgga 720
gatagaggca actcccaggc cagtgcgctt tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaacct cctttccgtg ccactggtga atagggattg 900
atgaatggga agagttgagt cagaccagta agcccgctc ggggttcctg aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080
catctgtatc agccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagttagca taatttgga 1320
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatatac 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaag tcaga tggaa 1440
agagcaactg aagtctaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60
tcagatatat aaatgagcac caaacactac aaagtgaac caacatggtt ctattaaaaa 120
ctcncctttg ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaatataa aaatctgcaa atgcatataa ttcatatcta ggctattctt cncatatagg 240
catgtcatta gatagacttt ctttctatcc ttccngagg natttttttg nggtttacnt 300
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
gtggc 425

<210> 359

230/292

<211> 232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(232)
<223> 5' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 359
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagggtgtctg gccagcttag 180
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
<211> 1431
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:prime r

<220>
<221> misc_feature
<222> (1)..(1431)
<223> camp responsive element modulator (CREM)
gene.

<400> 360
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
tgcatgtgag tgagatcagg caccagaaga ggctccccag ctgtaactct agtgcagtta 180
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
cagtcacatc aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
atatatcaga ctacgacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540
tctaaccacg gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600
gctcctccac cagtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
cagttctttg tcccaggcag ccagggtgtt gtccaagctg ccaactggtga catgccaact 720
taccagatcc gagtcctac tgcgtgcttg ccacaggagg tgggtgatggc tgcacgccc 780
ggaagtttgc acagtcccca gcagctggca gaagaagcaa cagcaaacg agagctgagg 840
ctaataaaaa acagagaagc tgcccgggag tgtcgcagga agaagaaaaga atatgtcaaa 900
tgtcttgaag atcgtgtggc tgtgcttgaa aacaaaaaca agactctcat tgaggaaactc 960
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
tttactctaa tcaaggcagg agatgcagca gtcctactta ttgccatgtg gacttgtggg 1080
aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140
tgttgttcca ggatgtggaa tgcagcgtga tcacacttac cgagcttact ttgatctgtt 1200
tgtcaatagc atgcaaaaaa tgctttgttt gccctttgct tctgcttttt ttcagggaag 1260
ctgccaaaag atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
cagtgctgga agtccagaac aagaagctta tagaggaact tgaaaccttg aaagacattt 1380
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca gggagaagct 60
gtaatttttc aaaaacagta aaagctgggt tctcctaaac tattttcctt gtggtagtag 120
agatcagtg gtcagaaaca actcctgacc atttggttcc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacaggtctc ccgctgttcc actggctcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggttgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggtccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gaggtactgg ggggaactgat gggggaactt tcac cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta gggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgct g gccttaagg 240
tgaataaggt ggtggtgact gttctgcaga gattttctca taagcaggtg gagcattggg 300
aaccacaggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363

```
attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatggtta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcgcat cctgacagtg atcctgggag tcttactgct catcggtgt tggatttga 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc                                     370
```

<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

```
agcagacaga ggactctcat taaggaaggt gtctgtgcc ctgaccctac aagatgccaa 60
gagaagatgc tcaacttcac tatggttacc ccaagaaggg gcacggccac tcttacacca 120
cggctgaaga ggcgctggg atcgcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300
acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcacctta gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtt tcctttggaa tgggttagga aaaatgcaag ccatctctaa taataagtca 540
gtgttataaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggatttctg 720
gggccatcca attctctttt acttgaaatt tggctaataa caaactagtc aggttttcga 780
accttgaccg acatgaactg tacacagaat tgttcagta ctatggagtg ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaagatcc 960
tatagctctt tttttttgag atggagtttc gcttttgttg ccag gctgg agtgcaatgg 1020
cgcatcttg gctcaccata acctccgctt cccagggttca agcaattctc ctgccttagc 1080
ctctgagta gctgggatta caggcgtgcg ccactatgcc tgactaattt tgtagtttta 1140
gtagagacgg ggtttctcca tgttggtcag gctgggtctc aactcctgac ctcaggtgat 1200
ctgcccgcct cagcctocca aagtgtctga attacaggcg tgagccacca cgcctggctg 1260
gatcctatat cttaggtaag acatataacg cagtctaatt acatttcaact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg                                     1524
```

<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcgtt aggccttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttacacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgttagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttgcgagttg aacaatgac actgacaca aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540
gggnggggat aacccc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agtttagaat gcagcctgga 60
cgtcagcaca gcatcttttg agatccgaag aagatcgtca cagaagagtt tgtgcgcaga 120
gggtacctga ttataaacc ggtgccccgt agcagtcagg tggagtatga gttcttcttg 180
gggccccgag cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300
gaggttgagg ctatcctcaa ttcaggtgct aggggttatt ccgcccccta agtagatctg 360
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta cccccaaagg agtagatg nc 420
aaggggccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcg gcaagtgtcg gcggcggctg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180
cagcggcagc agcttcttac ggtataaagc tgttgcttcc tgaagaggct acaagcatcc 240

234/292

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcaactgccca agcacaaaag ccttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggctctggaa agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatccttg gagatccgaa gaagatcgct acagaagagt ttgtgcgcag aggttacctg 720
atttataaac cgggtgccccg tagcagtcgg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttccggtttg tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgatc tctttttatt ttcgattgc ttatca 1476

```

<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaaatca caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat caggggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaata taaaagtcac ccacactcag ccacgtgatt ggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 369

```
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa tttgtctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccggtc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
gacccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnngc agtggngttt gtt ttgtgtt tttt 414
```

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370

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ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249
```

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371

```
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtgggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgag gttagagagga aacttggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atggcaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaatct atactggata 660
tgttaacaaac cttacaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780
```

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ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta ttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatattt ctttgccctt ataactttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaa aaaaaaaaaa aa 1702

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 372

gtaggcagta tgattccaaa agttaaataa tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcctt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctgaaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgcnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng 585

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 373

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

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acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtataaaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcatcagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttattc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g 451

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c ttgggtgc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aaggggcaaaa tggaccatt 300
caaatttcct cccagggacc aggccctatt aaccctggga aatgtcctta gctggtgggg 360
gaaagggttg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
accog 425

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

ggcgttccag ttcccacttg gaggcnttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttcctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttgggg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaaagct attta tctgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gtcagtcct ttgatcagta taaattttt aaagttactt ttgtcagagg caccaaaggg 420
tttaaaactga ttcataaata aatatcngga cttcctcgtat cttccaaaaa aaaaaaaa 478

238/292

<210> 376
<211> 1794
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1794)
<223> cd44 antigen (homing function and indian
blood group system) (CD44) gene.

<400> 376
ccgcgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcacg ca gcctggggg 60
actctgcctc gtgcgcgtga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
aggtgtattc cagctggaga aaaatggctg ctacagcatc tctoggacgg aggcgcgtga 180
cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
catcggattt gagacctgca ggtatgggtt c atagaaggg catgtggtga ttccccggat 300
ccaccccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360
ctcccagtat gacacatatt gcttcaatgc ttcaagctcca cctgaagaag attgtacatc 420
agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480
tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
caaccctact gatgatgacg tgagcagcgg ctctccagc gaaaggagca gcacttcagg 600
aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
tgggggggtc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
catcttggca tccctcttgg ccttggcttt gattcttgca gtttgcattg cagtcaacag 900
tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcattt 1020
ggtgaacaag gactcgctcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
cctgcagaat gtggacatga agattgggtg gtaacaccta caccattatc ttggaaagaa 1140
acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380
ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440
tccccacca gctaaggaca tttcccaggg ttaatagggc ctgggtccctg ggaggaaatt 1500
tgaatgggtc cattttgccc ttcataagcc taatccctgg gcattgcttt ccactgaggt 1560
tgggggtgac tagttacac a tcttcaacag accccctcta gaaatttttc agatgcttct 1620
gggagacacc aaagggtgaa gctatttatc tgtagtaaac tatttatctg tgtttttgaa 1680
atattaaacc ctggatcagt cctttgatca gtataatttt ttaaagttac tttgtcagag 1740
gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. cyclin-dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 377

ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctggtggttt catttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatcct gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgcctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcaggt tgtaagcnc tccattattt 420
cacagcagct ggccatgctn ggagtccccc ca 452

<210> 378

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 3 (cdk2 -associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378

ggcacgagcg gcaactggtc tcgacgtggg gcggccanga ctgaagccca ngnttcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttcagggtt gtaaatTTaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatTTgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttcttg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

<210> 379

<211> 639

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(639)

<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379

atggagccgc ccagttcaat acaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttcagggt tgtaaatTTa aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatTTgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttcttg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

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tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tcctactata cctgtctgac 480
 acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
 cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
 tcatcaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
 attggatcaa ctatttcttc agatcgttct gattcagagc gagaggagat tgaagtggat 120
 gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
 gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240
 gtgtcaaaat ttcatctact tcatagaacc cagcatgaca taacagtgc gggaaaatat 300
 tcaactgggc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
 aaaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
 caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
 catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgctgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60
 ttcttttttt tttttttttt tttaagtaat taagggtagt taaattatatt aaagtataca 120
 aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180
 gaggcccccg tcgccaccgc cgggtgccat ggagcgggtg aagatgatca acgtgcagcg 240
 tctgctggag gctgccgagt ttttgagcgc cggggagcga gagtggaac atggctacgc 300
 ctcttcattc cgtccatgc cgagcccccg actgcagcat tcaaagcccc cacggagggtt 360
 gagccgggca cagaaacaca gcagcgggac gagcaacacc a gcactgcca acagatctac 420
 acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
 agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
 agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
 gaatttggaa cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctccta 660
 ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720
 ttacagagcga gaggagattg aagtggatgt tgaaagcaca gagttctccc atggagaagt 780
 ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 840
 tgggagtgac gagggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

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agcatgacat aacagtgcag ggcaaaatat tcaactgggc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatgc agtctcctct ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgaacaa aaggggcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcatacta cattgagtag acacatttaa 1260
ggatgggggt atgaaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctc gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaacctt 1560
atcctgcatt gtttagcata ggcaaccagc tgccacctct ccatcctgct gcccttaggc 1620
cacatgggag cagtcacatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
gggggggcaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aacccaaatg acatctttt aaagcttata cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat tttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtgaaaaaag ggtcaatgct atttttgttt ttagaatcat tacctttttac 2040
cagcttttaa ccacttgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt acatttttaa tgtaaagatt tgcttcatt ttctacagg cagtctctct 2160
cttctcaca gtccactgt gcagggtgta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcattgtgt cctttgtct 2280
ttcaaaactcc aaggttcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac ttaaataat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa
2416

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<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 382

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ttttttttt ttgttatagt tacttcaagt aacacagctt gcttcatata aataagttaa 60
aacatctatt ttttttcaag acaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac aggccttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggatc cgctaaatac tgctcagtag tttaaacgct cagatactca 300
gggacggaag gccctccctt gcccgcggn c atnctccatg gcttttcagc ttattatc tt 360
tttccactt caatcncc
378

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<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
 <222> (1)..(439)
 <223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383
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 cgctatccaa atggcccgga ctaccagttg cataattatg gagatcatag ttccgtganc 120
 gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180
 atggatctca gcgtcggcng ctcgngctcc ngcacttttg ctccggagag cgcgcccgc 240
 gctacgtnc aagcgcacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300
 acgcactctn cctcancncg atccgctgcn ctgctccgnc gtnggcccct tcgcccngga 360
 ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgcctcgggc 420
 cgacngccgg aagcaccca 439

<210> 384
 <211> 813
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(813)
 <223> homeo box a5 (HOXA5) gene.

<400> 384
 atgagctctt atttgtaaa ctcatthttgc ggtcgctatc caaatggccc ggactaccag 60
 ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
 cactccggca ggtacggcta cggctacaat ggcattgata tcagcgtcgg ccgctcgggc 180
 tccggcact ttggctccgg agagcgcgcc cgcagctacg ctgccagcg cagcgcggcg 240
 ccgcccagc ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
 ctgccctgct ccgcccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaac 360
 tccctaagca actccagcgg cgcctcggcc gacgcgggca gc acccaccat cagcagcaga 420
 gaggggggtg gcacggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480
 agtgccgaga gcgagccgag cccggcgccg cccgcccac cccagatcta cccctggatg 540
 cgcaagctgc acataagtca tgacaacata ggcggcccgg aaggcaaaa ggcggggacg 600
 gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
 accgcagaa ggaggattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720
 atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
 atggccgagg caggaggggc cttccgtccc tga 81 3

<210> 385
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 3' terminal sequence. x-box binding protein 1 (XBP1) gene.

<400> 385

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```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cctttcagaa 60
gctacactag caggaaaaaa ttccatcaag cattttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcaggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaattgac ccttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttcntacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc                                447

```

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 386

```

aagaacctgt agaagatgac ctcggtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tccctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttccctttc ccatttcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccctgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagttaa gaaattattac tnataattgg ag                                462

```

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

```

ggcgctgggc ggctgcggcg cgcggtgcmc ggtgcgtagt ctggagctat ggtgggtggtg 60
gcagccgcgc cgaaccgcgc cgacgggacc cctaaagtct tgcttctgtc ggggcagccc 120
gcctccgcgc cggagcgcgc ggccggccag gccctgccgc tcatgggtgc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgcgt aggaggaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgcgc tggaacagca agtggtgat 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggccttgtag ttgagaacca ggagttaaga cagcgccttg ggatggatgc cctgggtgct 480
gaagaggagg cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtcc 540
gcagcactca gactacgtgc acctctgcag caggtgcagg cccagttgtc acccctccag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatcctgt 660
tgggcattct ggacaacttg gaccagtcga tgttcttcaa atgcccttcc ccagagcctg 720

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ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcatcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaatc gaggaagcac ctctcagccc ctgagagaat gatcaccctg 960
aattcattgt ctgagtgaag gaagaacctg tagaagatga cctcgttccg gagctgggta 1020
tctcaaatct gctttcatcc agccactgcc caaagccatc ttctgccta ctggatgctt 1080
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tctaaggaat gatccaatac tggtgccctt ttcttgact attacactgc ctggaggata 1260
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gcagtccaag gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
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gtaagatcaa gaatcttttg tgaattata gaaatttact atgtaaat gc ttgatggaat 1740
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caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaagtgt gactcttggt aaaagttaca tttattttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaagtgtc 120
aaatttcaa tacittttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttta gagaattaga tgaaaacact 240
gaagtgttatt tgngtatcct tggaaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggccont aagtacagac cccnnaatg gcagcctta tcnccgggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatngnn cctctt 206

<210> 390
<211> 4426
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4426)
<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390
tgccttgacc aggacttggg acttttgcga aggatcgagg ggcgggaga ggtgttgagg 60
agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat gcggaaagct 120
gtgaagatac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
catttttaaaa ccatgcacgg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gaacttggtac tgaggaaggg gctgttcagc a cgtcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaaatata catatttgtc 660
ctttgcaaca tctcagaag gccaatcatt gtcatttcag aaaaatgct aagaagtttg 720
gaatcaggtt ccaatttcgc ccctttgaaa gtgggtggaa tttacttgcc tctccactgg 780
cctgcccagg aatgctacag ataccocatt gtctcggct atgacagcca tcattttgta 840
cccttggtga ccctgaagga cagtgggcct gaaatccgag ctgttccact t gtaacaga 900
gaccggggaa gatttgaaga cttaaaagtt cactttttga cagatcctga aaatgagatg 960
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ccaaccaga ggatgggcc tggggccac cggggtgagc ctgccccga agaccccccc 2340
aagcagcggt gccggggccc cgcctgtgat cattttggca atgccaagt caacggctac 2400

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tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaacagag tgggtcacct 2460
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taaaaaatta gaatatatta ctgggaagac gtgtaactct ttgggttatt actgtcttta 3180
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taaattgaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

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<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

```

ttttttgtg caaaaaatg atacatttat tgaaagagta tttttttttt aatacaaaaag 60
aaagctctgt acataggact gtgaccatgt ccactattcc tgggtcagca tcccagggga 120
agtagaaaac actgacatac aactcacat tcaagcacac aactcactc aggcgcacac 180
accacacac acatacccca gagccacoga ggaagggaaa caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgatgtcc tcccaaggcc acgctcacac 300
aacacacatt ataagcactt tgctgattc actcactngg gtctgtcttt tgtgggaagg 360
agaggaagaa ttcatcaaag gtctcctccc catgggtngg gggagtgggg agtgagttag 420
tgatggtgga gtgaaacaag

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440

<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60
tgcagcaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaatt aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taatttgtac agggggccatg ccacncccc tcctcccctc ttgngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaathtt 360
cttaaccctt aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
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ccgcggccag cagcccctgc ccccggggg acgctgacgg ccgcccggcg cgccgcccta 120
gcagacggac agggggcgct gcgcggggcc tggggcaacc cgggccac ag gggcaggaaa 180
gtgagggcc aggtcggccc gggcgtgcag gggccccggg ttgcagcgg cgcccgcggc 240
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tgaagagaca gatctcacct accaggtgtc ggagtctgac agcagtggg agaccaagga 1140

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cacactgaag ccggcggttca cagtcaccaa cctgccgggt acaacctcca ccatccaaac 1200
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agaaacaggg cagcagtggt gtgaaatttt cttaacccct aagactgcct tcagtaggaa 3480
caagctggct tctgtgatta ggtgaaggga ttggggaaga ttttatgcac agcctagtta 3540
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tatttttatg tgcagcgacc cttggtgtt cccttctcg gtgctctgg ggtatgtgtg 4020
tgtgggtgtg tgcgctgag tgagtgtgtg tgcctgaatg tgagtgtgta tgtc agtgg 4080
ttctacttcc cctgggatgc tgaccagga atagtggaca tggtcacagt cctatgtaca 4140
gagctttctt ttgtattaaa aaaaaatact ctttcaataa atgtatcatt tttgtgcaca 4200
g 4201

```

<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>

<221> misc_feature

<222> (1)..(563)

<223> 3' terminal sequence. sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9) gene.

<400> 394

```
tttttaatgc aatgtatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaaa ggtaagtttc acggagagaa caaaaggttt ggggctggga gggaaacaag 120
tgaacaaaac aaaacacgaa cacaaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccaggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgcttta agattttatt ctactgactt ctaaaactgt 300
taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taaggctgtg cagtgggctg atcccctcca 420
ggtagcctcc ctcaactcaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttgtg nccaaacaca cacanacca nacacacnca caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa                                     563
```

<210> 395

<211> 3936

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3936)

<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395

```
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gtttcaaccc cggaacttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120
cttttgctct ttttctccc ctctcctcc tctccaattc gectccccc acttgagcgc 180
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggtg gccggc cgac 240
gcgccagctt ccccgggagc cgcttgctcc gcatccgggc agccgagggg agaggagccc 300
gcgcctcgag tccccgagcc gccgcggctt ctgcctttc ccggccacca gcccctgcc 360
ccgggcccgc gtatgaatct cctggacccc ttcatgaaga tgaccgacga gcaggagaag 420
ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgccc 480
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gagcccgatc tgaagaagga gagcgaggag gacaagtcc ccgtgtgcat ccgcgaggcg 600
gtcagccagg tgctcaaagg ctacgactgg acgctgggtc ccatgccggt gcgctcaac 660
ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtggcg 720
caggcggcgc gcaggaagct gcgggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc ctctgtggag 840
gaggcgagc ggctgcgcgt gcagcacaag aaggaccacc cggattacaa gtac cagccg 900
cggcgaggga agtcggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaacgccat cttcaaggcg ctgcaggccg actcgccaca ctctcctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080
ccaccacca ccccaaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140
cgcccttgc cagagggggg cagacagccc cctatcgact tccgcgacgt ggacatcggc 1200
gagctgagca gcgacgtcat ctccaacatc gagaccttcg atgtcaacga gtttgaccag 1260
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggt cacctacag 1320
ggcagctacg gcatcagcag caccgcggcc accccggcga gcgcgggcca cgtgtggatg 1380
tcaaagcagc aggcgcgcgc gccacccccg cagcagcccc cacaggcccc gccggccccg 1440
```

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```

caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
ccacagggcg acacgctgac cagcgtgagc agcgagccgg gcca gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgcgccaa 1620
cagatcgctt acagccctt caacctccca cactacagcc cctcctaccc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcgga 1740
ggccagggca cggcctct a ctccacctt accatcatga acccgctca gcgccccatg 1800
tacaccccca tcgccgacac ctctggggtc ccttccatcc cgcagaccca cagcccccag 1860
cactgggaac aacccgtcta cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgagcagtg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca ttgtgtttt ttgtttttt tattttgtt tgttttttt tcttcttctt 2040
cttccttaaa gacatttaag ctaaaggcaa ctctgaccca aatttccaag acacaaacat 2100
gacctatcca agcgcatlac ccacttgttg ccaatcagtg gccaggccaa ccttggctaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgttg 2220
aggatgatgg agaatcgtgt gatcagtggt cttaaactct ctgcctgttt ggactttgta 2280
attatttttt tagcagtaat taaagaaaaa agtcctctgt gaggaaatatt ctctatttta 2340
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tttagataaa attaaatgct cttatttttt caacagctaa actactctta gttgaaacagt 2460
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agaaaaaaa aatcctgttg tattaacatt taaaaacaga attgtgttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
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gtaagcttta tgatatatat attttttaaa gaagagaaaa acaccttgag ccttaaaacg 2760
gtgctgtcgg gaaacatttg cactctttta gtgcatttcc tctgccttt gcttgctcac 2820
tgagctctta agaaagaggt aaaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcc cgagcacact gcccccggtt gcctgcctgg gccccatgtg 2940
gaaggcagat gcctgctcgc tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacattc cacttgctaa aattatttat tttgtaagga gaggttttaa ttaaaacaaa 3060
aaaaattct ttttttttt tttttttcca attttacctt ctttaaaata ggttgttgga 3120
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aacaactgg aaactgttt cttttttgt ataatgaga gattgcaaat gtagtgtatc 3360
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ctacatcttc tcttgagtg agggaggcta cctggagggg atcagcccac tgacagacct 3540
taatcttaat tactgctgtg gctagagagt ttgaggattg ctttttaaaa aagacagcaa 3600
actttttttt ttatttaaaa aaagatatat taacagtttt agaagtcagt agaataaaat 3660
cttaaaagcac tcataatatg gcaccttca atttctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tattttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgt tcaactgttt cctccaccg cccaaacctt 3840
ttgttctctc cgtgaaactt acctttccct ttttctttct cttttttttt ttgtatatta 3900
ttgtttacaa taaatataca ttgcattaaa aagaaa 3936

```

<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggagg 60
tgctgtcttt canacaaaga tgagggtcac tggaggagg caaagggtgg actaggagg 120

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tgaccgcgcat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgccgccac ttccgagaga tgccccgcag ncagcctgca ccccagcca ccccgagtgc 120
tgcccaccag ccccttgac atcgccgact tcatcaatga tggcttga g gctgcagata 180
gtgacccag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cggtgccggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc ccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggtct ttctctggg 420
gcactgctac ccagacacag aggcgggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgcgctg tcaactcagcc tggacgcgct tcttcgggtc gcgggtgcac tccggcccgg 60
ctcccgcctc ggccccgatg gacgcgcgct tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccacctg taccctggc 180
gccgggcgcc tgccctgagc cgcgtgcgga gggcctgggt catcccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtccggac aagcagcagc 300
tgggcagcgt catctacagc atccagggac ccggcgtgga tgaggagccc cggggcgctct 360
tctctatcga caagttcaca gggaagggtct tctcaatgc catgctggac cgcgagaaga 420
ctgatcgctt caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaattgaaa ccggccagcc ttccctgcag 540
aggcgttcac tggccgcgtg ctggagggtg cagtcaccag cac ctatgtg accagggcag 600
aggccacaga tgccgacgac ccgagacgg acaacgcagc gctgcgggtc tccatcctgc 660
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aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

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```

ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggc actctgggtg 1260
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cccaggatga cgccctccag ccccgccagg ccaccggcac cctgtccatc gagatcctg 1500
aggtgaacga ccatgcacct gtgtggccc cgccgcggcc gggcagcctg tgcagcgagc 1560
cacaccaagg cccaggcctc ctctggggc ccacggatga ggacctgcc cccacgggg 1620
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gccaggtaaa cgtgagccac gcgcgcctgc ggccgcgaca ccaggtcccc gaaggcctgc 1740
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tgaacgtgac cgtgtgcgc tgcggcaagg acggcgtctg cctgccgggg gccgcagcgc 1860
tgctggcggg gggcacaggc ctacgc ctgg gcgcactgg catcgtctg gccagcgccc 1920
tctctgtctg ggtgtgtgct ctgtctgtgg cactccgggc gcggttctg aagcagtctc 1980
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gctgcaccc ccagccacct cgagtgtctc ccaccagccc cctggacatc gccgacttca 2220
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gacctgggg cgcaactgga catgccactc cccggcctcg tggcagtgat ggcccctgca 2580
gaggcagcct gaggtcaccg ggcccagccc cctgggcct ggggcagcct ccttctgtga 2640
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ccttctgcc ggggtgggaa gaggtttctt ccateggccc catgcgggtc acc tccctag 2760
tccacacctt gcctctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

```

<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 399

```

tatctcacac tgtactttat ttttcttcac aatattaact agacagacaa ggaaagttaa 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtgcca 120
actggagact tactttacct taacctatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttgtag aatatcagcc acctcttaaa agtatcaatc ttaaaaaagag ccatggaagg 240
taaaagtatg aaaaacttga taacaaaagc tttcaatata aaaacactta ttgtacactt 300
atthttatth aaaaacaaaa taac cccagt aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaa cttcccaaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggcca cgagatthtt ccaaaaggth taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctacaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

```

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<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 400
ggtattttaa caataaatgt gcagttttta ctaacaggat atttaatgac aaccttcttg 60
ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataataca agtccttttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaagg ctctgacaca 60
tgcacacgct cctgggacag cctgctgcgn gtncgcttcc catga ccccc agggccctct 120
atgcctcccc cccagggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggtc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcancogg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402

```
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttatttaaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgaggggtct ccgcatttat tttcaaggcc aaaggaagtg 180
acccttcgga aaacaaccctc gcacaacaaa gggcttcag aatctccatt gcacgagtct 240
cttccacctc ggaggtcttc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcaactca 360
gagtatcggg acccaagatg cactattggg gagtcctgcc ccaccctggc aacttggcac 420
atggttctctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggttatttt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568
```

<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403

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cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcttgctaat tcctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtta agaaagagt tcc ctatcca tgctatgacc 360
cagccacacg cgaaggtgac cttaaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagtgc aggggtggggg aggactcaca atagtgcac ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
acctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgagg gtcacttcct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctotcaa 780
agaaacacct caactggata attatgacta tcaaggagc agtttaata accgtttcct 840
ttcatttact gtggcttctt aatcttttca caaataaa 878
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<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404
gcagtgcacg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgccctcgg 60
cccctcgccc ggctttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcatc ctcccgtgc agcagcgct ccccgccgg gataantctc ctttattaca 180
attaatcanc g 191

<210> 405
<211> 245
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(245)
<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405
ttttcaactt aaatgctttt attgacaatg ttttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
ttcatggaaa actgttaatg tcngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245

<210> 406
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406
gcnccgcgt caccgaagg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaaaat ttgcccagg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggta 300
gtcccggcag ttccttccc gcactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgtccg tccacctgtc cagcggagcc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcc a gtagacttc gtctgaactt 480
gaacaagac 489

<210> 407
<211> 247
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

```
tggtttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcacc tgcacatttc cgtgttacag cagctgcctg atgaa ttta tccacctcca 120
tttcagcatg tggctgcgct ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccacagga cgagccagtg ccgggaagga actgccggga ctaccganc tgcncttaac 240
tggtctc                                     247
```

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

```
gcccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60
gctcgctcgc tcgcccggcg gcctcgcctc ggccccctcc ctacagctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gcctcggcgc gccaccggcg ccgcgcgga gcggcccggg 180
ggccctcacc caggcccatg gcggcgcgcg ggccgcgctct cgggcccggc accacgcggg 240
cgcgggggcg ggggcgcggg gcccggggcg ggtcccgcgc ggcgctgggc cgtggggcgc 300
ctggaggggc gcgagttcga gtatctgatg aagaagcgct cggtgacct cggccgcaac 360
tcgtcgccag gctcggtgga cgtgagcatg gcccactcga gttcatctc ccggcgccac 420
ctcgagatct tcacgcccc gggcggcgcg gccatggcgg ggccgctccg gagctgcgc 480
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tgtgcacatt cagggtcccg agcacaaca tcaagataac gttactgcc ctgtccagcg 660
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cctgcacct ccagccacc gtcgtgcaga cggttcacgt cgtccaccag atcccagcgg 1620
tgtcggtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680
```

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```

ctgtggtcac cccggcagcc gtgctggccc ctctaaggc agaggcccag gagaatggag 1740
accacagggg agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcactgccag ccggatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacaggc acctctaggt caacaccagc taccaataaa aactgtaaca caaacaggca 1920
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```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 409

```

tttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggt cccttggttg ttcttggtg ggtcaggga 180
ggcctgccgn ggtggtggc a

```

201

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 410

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ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120
tgtgtgctc cggggtggan ctggggtgtg ggatgcacgg cctogtgggg gccgggcccgt 180
cctccagccc cgtgtctccc tggccagccc cc ttgtcgtc gtcgggtccc tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

<210> 411

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha
(ARHGDI A) gene.

<400> 411

cctgaaccgc gcggccgaac cctccgggtg cccgaccag gctaagcttg agcatggctg 60
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120
actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
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cagaccacca cgtccccaac gtcgtggtga ctggcctgac cctgggtgtg agtcgggccc 300
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accaagtgc cactattgct agagccgtct cctataggtc ccccgcccca tccccggtgt 1740
tggtgtgtg tctgccaggc tcaggcagag gcgctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

<210> 412

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtctcca gcttcatggg tcccagggtc aggttcctcc cagcggagggt gggagggcag 120
ccctcacacc tggcaccctt gactgcatac tcttgaggga agtcgttgag ctgggcacag 180
gtgcccgcgt ggcgggttgc tccggcacag gcgttcagag ggcattctct cgatccagct 240
attcgagtc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
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```

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<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
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<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
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gcagaagcca aaaaatcac atggttttaa gatgggaaga tgatcggtt ctaactgaa 120
gataaaaaa aatggaatct gggaagtaat gccaaggacc ctgagggat gtatcagtgt 180
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aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

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<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

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<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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gccgccccca aaggccgct 43 9
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<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

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(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418
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cccgttcctc ccgccgtcag ccctgctgcc agaccctgac ttcttctctg ggcaccgtgt 180
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<210> 419
<211> 2314
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2314)
<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419
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<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
 (ESR1) gene.

<400> 420

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<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
 (ESR1) gene.

<400> 421

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<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6450)
<223> estrogen receptor 1 (ESR1) gene.

<400> 422
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<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 423

```
ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg gccaggggaag atgacgaaaa ccaggctgac agctggaggc agggaagggg 180
ggcttctacc cagaaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg tttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgcccct gcccactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggtat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaaggg gtagtagcat cctgcccaacc 480
tcattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccaggtatc acaactgggt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgctgcc aaaacagctg tctgtgtac caatgtgtca gccatggaa gccaaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttcg ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgttaa 300
tggaggttgg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgac tcccagcaat cgcacccgg ctgaccctgt 420
gccccagttg gccaggggca ggaggaggg tttctctccc aacgtgaag cggtcagact 480
ggaggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1
(PBX1) gene.

268/292

<400> 425

```

cttcctgtt tctctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggctgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggctgggat ggccggacac 180
cccgccctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gagcgcgagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttgtgtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcggctggac aacatgctgt tagcggaagg cg tggcgggg 480
cctgagaagg gcggagggtc ggcggcagcg gcggcagcgg cgcgggcttc tggaggggca 540
ggttcagaca actcagtggg gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagc caggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagcga aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttccga tttctggatg cgcgggcgaa gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccagaagt gtggcatcac agtctcccag 960
gtatcaaaact ggtttggaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
gaggaagcca atatttatgc tgccaaaaca actgtcactg ctaccaatgt gtcagcccat 1080
ggagccaagc ctaactcgcc ctcaactccc aactcggctg gttcttcca g tctttttaac 1140
atgtcaaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
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ggccctggca gtgttctact tgatacctcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc cccagttggg gcaggggcag gagggagggt ttctctcca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct ttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg ttttcgtcat cttccctgcc 1680
cctgtgcctc tgtcctagac ttcccggggg ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli -kruppel family
 member gli3 (greig cephalopolysyndactyly syndrome)
 (GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tacttttagg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttagggtgag tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaaagtc agtttaatct cttcaactcc taatgatttc cgttggttgc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aacctatgga aaaggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctgttacc ctccaggcc aggtcg 506

```

<210> 427
<211> 239
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(239)
<223> 5' terminal sequence. gli-kruppel family
member gli3 (greig cephalopolysyndactyly syndr ome)
(GLI3) gene.

<400> 427
ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
tgtctctatt taaaaaaciaa aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120
ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
agagacaggg ttccaccacg ttgcccaggg cagtcttgaa ctctgaccc caagtgatc 239

<210> 428
<211> 5054
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5054)
<223> gli-kruppel family member gl i3 (greig
cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60
gcccagtcac acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
tgctccactc gaacagatgt gagcgagaaa gccgttgccct ccagcaccac ttctaattgag 180
gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
ccgtaccgcg ggacgggtg tt tgccatggac cccaggaatg gttacatgga gcccactac 420
caccctcctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
gagggccgtt accattacga tccatctccg attcctc

cat tgcatatgac ttccgcctta 540
tctagttagc ctacgtatcc ggacctgcc ttcattagga tctccccaca ccggaacc cc 600
gctgctgctt ccaggtctcc cttcagccct ccacatccct acattaatcc ctacatggac 660
tatatccgct ccttgccacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
agccctacag atgcgcccc a tgcaggagtc agccacgag aatactatca tcagatggcc 780
ctgctaactg gccagcgcag cccctatgca gacatt attc cctcagctgc caccgcccgc 840
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agccctgcct tgagcttcac ctactctcc gogcccgctc ctctccacat gcacagcag 1140
atcctaagcc gacaacagag cttagggtca gcctttggac acagccctcc actcatccac 1200
cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggcccc ttctgagttcc tcacagaaca agcccacgag tgagtctgca 1320
 gtgagcagca ctggtgaccc gatgcacaac aagagggtcca agatcaaacc cgaatgaagac 1380
 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgctcaag 1440
 gaggaagggg acaaatgatga aagcaaa cag gagcctgaag tcatctatga gacaaactgc 1500
 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttggtgca ccatataaat 1560
 aacgaccata ttcatggaga gaagaaggag ttctgtgtgca ggtggctgga ctgctcaaga 1620
 gagcagaaac ccttcaaagc ccagtatatg ttggtagtgc atatgagaag acacacgggc 1680
 gagaagcctc acaaatgcac ttttgaaggt tgcacaaagg cctactcgag actagaaaac 1740
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 tccctccgga aacatgtgaa gacagtgcac ggcccagagg ctcatgtcac caagaagcag 1980
 cgaggggaga tccactcctc gccgccaccc ccgagagatt ccggcagcca ttcacagtcc 2040
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 gccttccatg aacagccctg taaggccccg cagtatggga actgtctcaa caggcagcca 3840
 gtggccctcg gtgactcga cggtgccctgt ggtgcgggga ttcaagcctc aaagctgaag 3900
 agcaccacca tgcaagggag cggggggccag ctgaatttcg gcctgccggt agcgcacaaat 3960
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 cagatgcttg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140
 tgctgccag gggctcacgg catgggcagc cagccgtcaa gcttggcagt tgtcaggggc 4200
 taccagccat gtgccagctt tgggggcagc aggcgcaggt ctatgccgag ggacagcctt 4260
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 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620
 ctgagcccaa gtatcattca gaacctttcc catagctcct cccgcctcac cagcctcgg 4680
 gcgtccctcc cattcccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc accttaactga 4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
agggagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaat ttgcccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcgggtga gtcccggcag 120
ttccttcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgtc cagcgagcc acatgctgaa atggagggtg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar t o NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432
ATTCGGCAGC ATGACTGGCC AGGGTATAAA AAGGGCCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTTCGGT TATCCAGGGT TTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACGAC GCCTGCCAGG GNATTTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                     247
```

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                     63
```

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

```
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCCTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                     190
```

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TAACTGGAC TTAACATAAA TGCACTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCTCG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAA TGTTCCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P, granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCCACG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTC AATAACAGGT GAGNAAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTTCTTGA GCTGCAGCTG GCGGTAGGG CNCGGGGCCC CGCGGGACGT 300
CCAGTACGAC CTGTA CTGTA ACGTTNCCAA CAGGNGT 337
```

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

```
TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104
```

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

```
AAGCAATGGA TGATTTGATG CTGTCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTCCGTCT G GG 223
```

<210> 443

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<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180
cttccagaa aacctaccag ggcagctacg gtttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggtg cagtgaggac 60
cccacagtac ccctgccctc tgagactgat ggctacgttg ccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cgccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccagact gctgggtgcca ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggg gccgtgggag aaccccgagt 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcatct tgcgccccct gctggtngaa 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc ccacttgct 240
ntcgaagggg ganttgggna ngtagggtn gtngtttgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tgttcacaac tataaatTTA 60
aaccttttgc actaaaaaaa cacaaaacaa caaacacaa accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180
tccttggaac ctgtaatgtt ttngcacggg ntgatctccc gcngggggta ctagtaatga 240
ctggctgccc gtgtaggagg atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448

<211> 393

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 3' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(393)

<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448

aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggtaaggga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa tttcacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atnccgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449

<211> 217

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(217)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(217)

<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449

ttacntgggt atctoctact gtagtatgag gaagaatggc tgttaatgta ttttttgaat 60
tctggnetca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120
tgtgccgaga attctacaa cgagc actgg aactacctga ccatctgcca nctgtgccgc 180
ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

<210> 450

<211> 157

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

```
nattcggcaa cngggaaagg aaagaaacta accaacaata gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca                               157
```

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis -related cysteine protease
(CASP4) (ex CASP1)

<400> 451

```
gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtctc ctgacagcac attcttggtg ctcattgtct atggcatcct ggagggaatc 120
tgcggaactg tgcattgatg gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcttcagtct ngaaggacaa acccaagggt atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgect 120
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggtcctc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttctgt gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaaggtgg gatgggcccc agcnacagct ttgnaccc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgcc cggtgcccc tcaccct gtg gcaagtacat ctctgcgcc gagtgcctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc 180
ctacacgtg gagcagcagg acgggatgga cgcctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcecca acatcgccgc catcgctcggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctctg ctggatcatc gggaaggctc tgatccacct gacgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtc cagtnngaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

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<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgn aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgnctgncc acggaggcct gttccccgga 180
cctgncagtt ctatgggnagc agattcggcg ggatcatgcg gccacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggaact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcactt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn                                     544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagaggaac 60
cggcgcgggc gngtgcngt aggcccggtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcggngggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggnaaga gccncagcga 240
gaangcnaaa gaaanccnga caaagaanc caacngcaa gaggnncgan gnccaggnac 30 0
ngnccngnga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456
cagcctcccg cgcctcgtc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatgggttata 120
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatggtca gctagatttc tcagaatttc ttaatctgat tgggtgccta gctatggctt 300
gccatggact ccttcctcaa ggtgtccct tccagaagc gggacctgga gggacccctt 360
gggccctggg cctttcaaac ccacccctn ttcctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttnctg gaggcacatt aaccacctna tggtagggtg ccaactggtc 480
attagttatt aaaggaatg tnaatttttt ttaa 514

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaccgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatggggcc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa agggcaaagg cagctctgca cctacttctt gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tnctaag aacctnaat 359

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

<220>

<221> misc_feature
<222> (1)..(1251)
<223> endothelin 1 (EDN1)

<400> 458

```
ggagctgttt accccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcccgc tgcgcctgca gacgtccgc tcgctgcctt ctctcctggc 180
aggcgctgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgcg agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgtgtg ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggtgg gtgagaacgg cggggagaaa cccactcca gtccaccctg gcggctccgc 480
cggtccaagc gctgctcctg ctcgctccctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggaaagccct 600
aggtccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggtcg aagacattat ggagaaagac tggaaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaag acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatg atcccaaagt gaaaggcaag ccctccagag agcgttatgt gaccacacaac 960
cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cgagagagccc 1020
tgtggccgac tctgcactct ccaccctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttcactg gcttccatca gtggtaactg ctttggtctc ttctttcatc 1200
tgggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251
```

<210> 459
<211> 2145
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2145)
<223> 3' terminal séquence

<220>
<221> misc_feature
<222> (1)..(2145)
<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

```
cggcagaact gggaccaccg ggggtggtga ggcggcccgg cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctctcatt ccctgcgccc 120
ccttctctc cggaagcccc caggatgggt aggtgggttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttcctggc tcggcccagt 240
cgcaagaacc aggggtgactt ctgcctctcc gtcagggtgg gggatcaggt gacctatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag cagggtgtgg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtaccc gctgaactgc tccgatccca ctagtgagag gtggtaccat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
ttctttgtgc gtgaga gcct cagccagcct ggagacttcg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgag accttcgaca gcctcacgga cctggtggag 720
```

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```

catttcaaga agacggggat tgaggaggcc tcaggcgcct ttgtctacct gcggcagccg 780
tactatgcc aagagggtgaa tgccggtgac attgagaacc gagggttga actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagttga gaggttgcag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccctt gaccacagcc gaggatcct gcaggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggagatggc gtggcaggag aacagccgtg tcatcgtcat gaccaccga 1200
gagggtggaga aaggccggaa caaatgcgtc ccatactggc ccgagggtgg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatggggtc ccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcagc cagggcccat catcgtgcac 1500
tgcagcgccg gcatcggccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atgggtcgg 1620
gcgcagcgct cgggcatggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gcccagttca ttgaaaccac taagaagaag ctggaggtcc tgcagtcgca gaaggccag 1740
gagtcggagt acgggaacat cacctatccc ccagccatga agaatgccca tgccaaggcc 1800
tcccgcacct cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtc gcagacaagg agaagagcaa gggttccctc 1920
aagaggaagt gagcgggtgt gtccctcagg ggccatgcct cagccctgac cctgtggaag 1980
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aaatggctgc atccccccca cctctccctg acctgtata tagccagcc aggccccag 2100
cagggccaac ctttctctc ttgtaaataa agccctggga tcaact 2145

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<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

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cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cggcgtgcc 180
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gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
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ggagaagcta ttatatattt ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
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<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

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caggagggag aggggcccgc gggtggcca tggagctgct gtgccacgag gtggaccggg 300
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<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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agctgctcaa gtgcgccatt gtgcattca tcaactacca ggacgatgcc gagctggcca 540
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aataacacag 3490

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<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
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cgaggacgac gacagagatg tggctctgca gatccacttc accctgatcc aggcgttttg 540
ctgcgagaac gacatcaaca tcctgcgcgt cagcaaccgc ggcgggctgg cggagctcct 600
gctcttggag accgacgctg gccccgcggc gagcgagggc gccgagcagc ccccgacact 660
gcaactgcgt ctgggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720
acttatttgt ttttgccggg aaagtcgcta catggatcaa tgggttccag tgattaatct 780
ccctgaacgg tgatggcatc tgaatgaaa taa ctgaacc aaattgcact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900
tgatgccaa gggctgagtg agttcaacta catgttctgg gggcccgag atagatgact 960
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc ccgggcgcgt ttccgggtgct ggcggctgca gccggagtgc 60
aacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcgatcaaa 120
ccagatgggg tccagcgggg tctgtgga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggcctggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggtctggga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360
 gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
 ggcaggaaca ttatacat gg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
 tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
 tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600
 ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gagggaaagc 660
 tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
 cttcctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
 agccggaatg gcatgggtctt gaagccccac ttccacaagg actggcagcg gcgcgtggcc 120
 acgtggttca accagccggc ccgtaagatc cgcagacgta aggcccgga agccaaggcg 180
 cgccgcatcg ccccgcgccc cgctcggtt cccatccggc ccatcgtgcg ctgccccacg 240
 gttcggtaac acacgaaggt gcgcgcggc cgcggttca gcctggagga gtcagggtg 300
 gccggcattc acaagaaggt ggcccggaac atcggcattt ctgtggatcc gaggaggcgg 360
 aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
 ctcatcctct tccccaggaa gccctcgccc cccaagaagg gagacagttc tgctgaagaa 480
 ctgaaactgg ccaccagct gaccggaccg gtcatgcccg tccggaacgt ctataagaag 540
 gagaaagctc gagtcatcac tgaggaagag aagaatttca aagccttcgc tagtctcgt 600
 atggcccgtg ccaacgcccg gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660
 gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttgaatc agtcgggcag 720
 tcatgctggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780
 actgctgtga cttcctcctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
 tggataatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
 aaaacggttt tcttgtggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgcgcga ctcttgacgc tggccccccg 60
ccaggccctt gtctccacgc ctgatgcccc tggccaccag aggaagtgg tgcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gtcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggtgtgtgc cctgacgatg gcctggagtg tgtgccact ggcagcacc aagtcggat 300
gcagatcctc atgatccgtt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaaa ggacagtgtc gtgaagccag acagggtgc 420
cactccccc caccgtcccc agccccgttc tgttcgggg tgggactctg cccccggagc 480
accctcccca gctgacatca cccatccac tccagcccca ggccccctctg cccacgtgc 540
accagcacc accagcgccc tgacccccgg acctgcggcc gccgtgccc acgcccagc 600
ttcctccgtt gccaaaggcg gggcttagag ctcaaccag acacctgcag gtgcccgaag 660
ctgcgaaggt gacacatggc ttttcagact cagcaggtg acttgctca gaggctatat 720
cccagtggg gaacaaagag ggcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccg 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggtgtgc cttaagttcc ttgcagcagg aaccactta ggtggacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgtggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tegtgcatt gttgccattg aaaacctgc 300
tgatgtcagt gttatctcct ccaggaatac tggccagagg gctgtgtgc a agtttgctgc 360
tgccactgga gccactccaa ttgctggccg ctccactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc caaggcttct tgtggttact gacccagggt ctgaccacca 480
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgtga acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaatgtgg tggatgctgg ctcggaagt tctgcgcag cgtggacca ttcccgta 660
acacccatgg gaggtcatgc ctgatctgta ctctacaga gatcctgaag agattgaaaa 720
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgct cctgagttca ctgtactca gcctgaggtt gcagactggg ctgaaggtgt 840
acaggtgccc tctgtgccta ttcagcaatt ccctactgaa gactggagcg ctcagcctgc 900
cacggaagac tggctgtcag ctccactgc tcaggccact gaattggtag gagcaaccac 960
tgactggtct taagctg ttc ttgcataggc tcttaagcag catggaaaaa tggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcacg atgactggcc aggggtataaa aagggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccactcaggg tctgtggca gtcacctag tggcaatggc 120
tccaggctcc cggaacgtcc ctgactctgg nttttgnoct nctctnactg ccctggnttn 180
aanaagctng tgccttccaa ancgttcctg tatccagggt ttttgaccac gctatgctnc 240

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